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OM protein - protein search, using sw model

Run on: April 15, 2003, 12:01:27 ; Search time 131 Seconds
(without alignments)
189.942 Million cell updates/sec

Title: US-10-017-372E-37
Sequence: 1 MAFSGRLPLPLMLLV.....GRKPVEQLSMIVRSCKS 407
Perfect score: 2159

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications-AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2030.5	94.0	390	9	US-09-214-592-26
2	1929.5	89.4	390	9	US-09-214-592-29
3	1914.5	88.7	390	9	US-09-214-592-33
4	1909	88.3	391	9	US-09-214-592-17
5	1903.5	88.3	390	10	US-09-756-283A-23
6	1893.5	87.7	390	9	US-09-214-592-28
7	1893.5	85.0	390	9	US-09-214-592-20
8	1835.5	85.0	390	9	US-09-214-592-23
9	1572.5	72.8	315	9	US-09-214-592-25
10	1262.5	58.5	455	10	US-09-756-283A-20
11	1139	52.8	447	10	US-09-756-283A-22
12	1047	48.5	373	9	US-09-214-592-32
13	871.5	40.4	412	9	US-09-214-592-31
14	868.5	40.2	382	9	US-09-214-592-34
15	868	40.2	383	10	US-09-756-283A-27
16	834	38.6	409	9	US-09-214-592-27
17	827.5	38.3	410	9	US-09-214-592-22
18	826.5	38.3	412	9	US-09-214-592-24
19	824.5	38.2	412	9	US-09-214-592-19

20	824.5	38.2	412	12	US-10-028-158-21	Sequence 21, Appl
21	824	38.2	414	9	US-09-214-592-21	Sequence 21, Appl
22	820.5	38.0	412	10	US-09-756-283A-25	Sequence 25, Appl
23	809	37.5	414	9	US-09-214-592-18	Sequence 18, Appl
24	809	37.4	414	10	US-09-756-283A-24	Sequence 24, Appl
25	808	37.4	412	9	US-09-214-592-30	Sequence 30, Appl
26	792	36.7	304	10	US-09-756-283A-26	Sequence 26, Appl
27	753.5	34.9	139	12	US-10-002-278-8	Sequence 8, Appl1
28	638	29.6	112	9	US-09-813-271B-2	Sequence 2, Appl1
29	638	29.6	114	10	US-09-813-398-13	Sequence 13, Appl1
30	638	29.6	114	10	US-09-813-459-22	Sequence 22, Appl
31	638	29.6	114	12	US-10-115-406-21	Sequence 21, Appl
32	638	29.6	115	9	US-09-859-211-47	Sequence 47, Appl
33	638	29.6	115	9	US-09-880-708-25	Sequence 25, Appl
34	542	25.1	116	12	US-10-115-406-24	Sequence 24, Appl
35	535	24.8	112	10	US-09-813-271B-8	Sequence 8, Appl1
36	504	23.3	112	10	US-09-813-271B-12	Sequence 12, Appl
37	504	23.3	114	12	US-10-115-406-25	Sequence 25, Appl
38	500	23.2	112	10	US-09-813-271B-6	Sequence 6, Appl1
39	500	23.2	113	10	US-09-813-398-15	Sequence 15, Appl
40	500	23.2	114	10	US-09-813-459-24	Sequence 24, Appl
41	500	23.2	114	12	US-10-115-406-23	Sequence 23, Appl
42	500	23.2	115	9	US-09-880-708-27	Sequence 27, Appl
43	493	22.8	115	9	US-09-859-211-49	Sequence 49, Appl
44	482	22.3	112	10	US-09-813-271B-4	Sequence 4, Appl1
45	482	22.3	113	9	US-09-813-398-14	Sequence 14, Appl

ALIGNMENTS

```
RESULT 1
US-09-214-592-26
Sequence 26, Application US/09214592A
Publication No. US20030027218A1
GENERAL INFORMATION:
APPLICANT: Yamasaki, Chotaro
APPLICANT: Shibata, Kenji
TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
FILE REFERENCE: 11060
CURRENT APPLICATION NUMBER: US/09/214, 592A
CURRENT FILING DATE: 1999-01-18
NUMBER OF SEQ ID NOS: 34
SOFTWARE:
SEQ ID NO 26
LENGTH: 390
TYPE: PRT
ORGANISM: porcine
US-09-214-592-26

Query Match          94.0%  Score 2030.5; DB 9; Length 390;
Best Local Similarity 94.8%  Pred. No. 9e+165;
Matches 386; Conservative 1; Mismatches 3; Indels 17; Gaps 1;
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QY	1	MAPSGRLPLPLPLMLLVLPGRPAAGISTCKTIDMELVKKRRIRAIKQILSKRLA	60
DB	1	MAPSGRLPLPLPLMLLVLPGRPAAGISTCKTIDMELVKKRRIRAIKQILSKRLA	60
QY	61	SPPSQGDVPPGPEAVLALYNSTRDVAGESVPEPEPADYAKFVTRLWESGNOI	120
DB	61	SPPSQGDVPPGPEAVLALYNSTRDVAGESVPEPEPADYAKFVTRLWESGNOI	120
QY	121	YKFKGTPTSLYMLFNTSELREAVPEPVLLSRALRLRLKLVQHVHVLKYKTSNDSWR	180
DB	121	YKFKGTPTSLYMLFNTSELREAVPEPVLLSRALRLRLKLVQHVHVLKYKTSNDSWR	180
QY	181	YLSNRLAPSDSEPMISFDYTGYYRQMLTFRREALTEGRLSAHSSDSKDNTHVEINGFN	240
DB	181	YLSNRLAPSDSEPMISFDYTGYYRQMLTFRREALTEGRLSAHSSDSKDNTHVEINGFN	240
QY	241	SGRGRGLATIHGNRRPFLLMATPRLERARQHLHSSRRRAALDTNSYPYDVPDYLALDTN	300

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Db 241 SGRGDLATIHGMRPFLMLATPLERAQHLSSRRR-----ALDTN 283
QY 301 YCFSTKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVALY 360
Db 284 YCFSTKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVALY 343
QY 361 NOHNPASAPCCVPALEPLPIVYVYGRKPKVEQLSNMIVRSCKS 407
Db 344 NOHNPASAPCCVPALEPLPIVYVYGRKPKVEQLSNMIVRSCKS 390

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RESULT 2
US-09-214-592-29

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; Sequence 29, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, CMOtoo
; APPLICANT: Shibata, Ckenji
; APPLICANT: Sato, Ctasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 29
; LENGTH: 390
; TYPE: PRT
; ORGANISM: ovine
US-09-214-592-29

```

Query Match 89.4%; Score 1929.5; DB 9; Length 390;
Best Local Similarity 89.7%; Pred. No. 3.5e-156;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

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QY 1 MAPSGRLPLPLPLMLVLTPGRPAAGLSTCKTIMELVKRRRIEIRQILSKRLA 60
Db 1 MPSSGLRLPLPLPLMLMLTPGRPAAGLSTCKTIMELVKRRRIEIRQILSKRLA 60
QY 61 SPSSQGDVPPGPLPEAVLALYNSTRDVAGESVPEPEPEADYAKETRYLWVESGNOI 120
Db 61 SPSSQGDVPPGPLPEALIALYNSTRDVAGESAPTEPEPEADYAKETRYLWVEYGKNI 120
QY 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLSRAELRLRLKLKYEQHVELYOKYSNDSWR 180
Db 121 YDKMKSSHSIYMFNTSELREAVPEPVLSRAVRLRLKLKYEQHVELYOKYSNNSMR 180
QY 181 YLSNRLAPSDSEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Db 181 YLSNRLAPSDSEWLSFDVTGVVROWLTHREEIEGFRLSAHSCSDSKDNTLQVDINGFS 240
QY 241 SGRGDLATIHGMRPFLMLATPLERAQHLSSRRRALDTNSYPYDVPDYLADDTN 300
Db 241 SGRGDLATIHGMRPFLMLATPLERAQHLSSRRR-----ALDTN 283
QY 301 YCFSTKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVALY 360
Db 284 YCFSTKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVALY 343
QY 361 NOHNPASAPCCVPALEPLPIVYVYGRKPKVEQLSNMIVRSCKS 407
Db 344 NOHNPASAPCCVPALEPLPIVYVYGRKPKVEQLSNMIVRSCKS 390

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RESULT 3
US-09-214-592-33

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; Sequence 33, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, CMOtoo
; APPLICANT: Shibata, Ckenji

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; APPLICANT: Sato, Ctasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 33
; LENGTH: 390
; TYPE: PRT
; ORGANISM: simian
US-09-214-592-33

```

Query Match 88.7%; Score 1914.5; DB 9; Length 390;
Best Local Similarity 89.4%; Pred. No. 6.6e-155;
Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;

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QY 1 MAPSGRLPLPLPLMLVLTPGRPAAGLSTCKTIMELVKRRRIEIRQILSKRLA 60
Db 1 MPSSGLRLPLPLPLMLMLTPGRPAAGLSTCKTIMELVKRRRIEIRQILSKRLA 60
QY 61 SPSSQGDVPPGPLPEAVLALYNSTRDVAGESVPEPEPEADYAKETRYLWVESGNOI 120
Db 61 SPSSQGDVPPGPLPEAVLALYNSTRDVAGESAPEPEPEADYAKETRYLWVEITNEI 120
QY 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLSRAELRLRLKLKYEQHVELYOKYSNDSWR 180
Db 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLSRAELRLRLKLKYEQHVELYOKYSNDSWR 180
QY 181 YLSNRLAPSDSEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
Db 181 YLSNRLAPSDSEWLSFDVTGVVROWLTHREEIEGFRLSAHSCSDSKDNTLQVDINGFT 240
QY 241 SGRGDLATIHGMRPFLMLATPLERAQHLSSRRRALDTNSYPYDVPDYLADDTN 300
Db 241 SGRGDLATIHGMRPFLMLATPLERAQHLSSRRR-----ALDTN 283
QY 301 YCFSTKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVALY 360
Db 284 YCFSTKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTOYSKVALY 343
QY 361 NOHNPASAPCCVPALEPLPIVYVYGRKPKVEQLSNMIVRSCKS 407
Db 344 NOHNPASAPCCVPALEPLPIVYVYGRKPKVEQLSNMIVRSCKS 390

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RESULT 4
US-09-214-592-17

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; Sequence 17, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, CMOtoo
; APPLICANT: Shibata, Ckenji
; APPLICANT: Sato, Ctasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 17
; LENGTH: 391
; TYPE: PRT
; ORGANISM: human
US-09-214-592-17

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Query Match 88.4%; Score 1909; DB 9; Length 391;
Best Local Similarity 89.5%; Pred. No. 1.9e-154;
Matches 365; Conservative 10; Mismatches 15; Indels 18; Gaps 2;

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QY 1 MAPSGRLPLPLPLMLVLTPGRPAAGLSTCKTIMELVKRRRIEIRQILSKRLA 60

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; CURRENT APPLICATION NUMBER: US/09/214,592A
 ; CURRENT FILING DATE: 1999-01-18
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE:
 ; SEQ ID NO 20
 ; LENGTH: 390
 ; TYPE: PRF
 ; ORGANISM: murine
 US-09-214-592-20

Query Match 85.0%; Score 1835.5; DB 9; Length 390;
 Best Local Similarity 85.0%; Pred. No. 3.4e-148;
 Matches 346; Conservative 15; Mismatches 29; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEALRQILSKRLA 60
 DB 1 MPSPGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEALRQILSKRLA 60
 QY 61 SPSPGQVPPGRLPEAVLALYNSTRDVAGSVEPEPEADYYAKEVTRVLMVDSGNOI 120
 DB 61 SPSPGQVPPGRLPEAVLALYNSTRDVAGSADPEPEADYYAKEVTRVLMVDRNNAI 120
 QY 121 YDKFKGTPHSLYMLFNTSELRVAVPEVLLSRALRLRLKLYEQHVELYOKYSNDSWR 180
 DB 121 YDKFKGTPHSLYMLFNTSELRVAVPEVLLSRALRLRLKLYEQHVELYOKYSNDSWR 180
 QY 181 YLSNRLAPSDPEWLSFDVTGVVQWLTREALEGFRLSAHSSSDSKDNTLHVEINGFN 240
 DB 181 YLSNRLAPSDPEWLSFDVTGVVQWLTREALEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 241 YLSNRLAPSDPEWLSFDVTGVVQWLTREALEGFRLSAHSSSDSKDNTLHVEINGFN 240
 DB 241 YLSNRLAPSDPEWLSFDVTGVVQWLTREALEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 301 YCSSTKNCVQVQLYIDFKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLA 360
 DB 301 YCSSTKNCVQVQLYIDFKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLA 360
 QY 284 YCSSTKNCVQVQLYIDFKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLA 343
 DB 284 YCSSTKNCVQVQLYIDFKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLA 343
 QY 361 NOHNPASAPCCVQALPEPLIYVYVGRKPKVEQLSNMIVRSCKS 407
 DB 361 NOHNPASAPCCVQALPEPLIYVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 8

US-09-214-592-23
 ; Sequence 23, Application US/09214592A
 ; Publication No. US20030027218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yamasaki, Cmotoo
 ; APPLICANT: Shibata, Ckenji
 ; APPLICANT: Sato, Cyasufumi
 ; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
 ; FILE REFERENCE: 11060
 ; CURRENT APPLICATION NUMBER: US/09/214,592A
 ; CURRENT FILING DATE: 1999-01-18
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE:
 ; SEQ ID NO 23
 ; LENGTH: 390
 ; TYPE: PRF
 ; ORGANISM: rat
 US-09-214-592-23

Query Match 85.0%; Score 1835.5; DB 9; Length 390;
 Best Local Similarity 85.0%; Pred. No. 3.4e-148;
 Matches 346; Conservative 14; Mismatches 30; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEALRQILSKRLA 60
 DB 1 MPSPGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRIEALRQILSKRLA 60
 QY 61 SPSPGQVPPGRLPEAVLALYNSTRDVAGSVEPEPEADYYAKEVTRVLMVDSGNOI 120

DB 61 SPSPGQVPPGRLPEAVLALYNSTRDVAGSADPEPEADYYAKEVTRVLMVDRNNAI 120
 QY 121 YDKFKGTPHSLYMLFNTSELRVAVPEVLLSRALRLRLKLYEQHVELYOKYSNDSWR 180
 DB 121 YDKFKGTPHSLYMLFNTSELRVAVPEVLLSRALRLRLKLYEQHVELYOKYSNDSWR 180
 QY 181 YLSNRLAPSDPEWLSFDVTGVVQWLTREALEGFRLSAHSSSDSKDNTLHVEINGFN 240
 DB 181 YLSNRLAPSDPEWLSFDVTGVVQWLTREALEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 241 YLSNRLAPSDPEWLSFDVTGVVQWLTREALEGFRLSAHSSSDSKDNTLHVEINGFN 240
 DB 241 YLSNRLAPSDPEWLSFDVTGVVQWLTREALEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 301 YCSSTKNCVQVQLYIDFKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLA 360
 DB 301 YCSSTKNCVQVQLYIDFKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLA 360
 QY 284 YCSSTKNCVQVQLYIDFKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLA 343
 DB 284 YCSSTKNCVQVQLYIDFKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLA 343
 QY 361 NOHNPASAPCCVQALPEPLIYVYVGRKPKVEQLSNMIVRSCKS 407
 DB 361 NOHNPASAPCCVQALPEPLIYVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 9

US-09-214-592-25
 ; Sequence 25, Application US/09214592A
 ; Publication No. US20030027218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yamasaki, Cmotoo
 ; APPLICANT: Shibata, Ckenji
 ; APPLICANT: Sato, Cyasufumi
 ; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
 ; FILE REFERENCE: 11060
 ; CURRENT APPLICATION NUMBER: US/09/214,592A
 ; CURRENT FILING DATE: 1999-01-18
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE:
 ; SEQ ID NO 25
 ; LENGTH: 315
 ; TYPE: PRF
 ; ORGANISM: bovine
 US-09-214-592-25

Query Match 72.8%; Score 1572.5; DB 9; Length 315;
 Best Local Similarity 88.9%; Pred. No. 6e-126;
 Matches 295; Conservative 9; Mismatches 11; Indels 17; Gaps 1;

QY 76 AVLALYNSTRDVAGSVEPEPEADYYAKEVTRVLMVDSGNOIYDKFKGTPHSLYMLF 135
 DB 76 AVLALYNSTRDVAGSVEPEPEADYYAKEVTRVLMVDSGNOIYDKFKGTPHSLYMLF 135
 QY 136 NTSLEAVPEVLLSRALRLRLKLYEQHVELYOKYSNDSWRILSNLAPSDPEW 195
 DB 136 NTSLEAVPEVLLSRALRLRLKLYEQHVELYOKYSNDSWRILSNLAPSDPEW 195
 QY 61 NTSLEAVPEVLLSRALRLRLKLYEQHVELYOKYSNDSWRILSNLAPSDPEW 120
 DB 61 NTSLEAVPEVLLSRALRLRLKLYEQHVELYOKYSNDSWRILSNLAPSDPEW 120
 QY 196 LSFDTGVVQWLTREALEGFRLSAHSSSDSKDNTLHVEINGFNSGRGLDATTI 255
 DB 196 LSFDTGVVQWLTREALEGFRLSAHSSSDSKDNTLHVEINGFNSGRGLDATTI 255
 QY 256 PFLLMATPPLERAOHLHSSRRALDTNTPYVDPYASIALDTNCFSTENKCCVROL 315
 DB 256 PFLLMATPPLERAOHLHSSRRALDTNTPYVDPYASIALDTNCFSTENKCCVROL 315
 QY 316 YIDFKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLAQYHNPASAPCCV 375
 DB 316 YIDFKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLAQYHNPASAPCCV 375
 QY 224 YIDFKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLAQYHNPASAPCCV 283
 DB 224 YIDFKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLAQYHNPASAPCCV 283
 QY 376 QALEPLIYVYVGRKPKVEQLSNMIVRSCKS 407
 DB 376 QALEPLIYVYVGRKPKVEQLSNMIVRSCKS 315

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RESULT 10
US-09-756-283A-20
; Sequence 20, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
; APPLICANT: Chernajovsky, Yuti
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LAP-mIFN Construct
US-09-756-283A-20

Query Match          52.8%; Score 1139; DB 10; Length 447;
Best Local Similarity 90.5%; Pred. No. 2,3e-99;
Matches 248; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 1 MAPSGRLRLPLLLPLMLLVTTPGRPAAGLSTCKTIDMELVKKRIEAIKGLSKRLA 60
D 1 MPPSGRLRLPLLLPLMLLVTTPGRPAAGLSTCKTIDMELVKKRIEAIKGLSKRLA 60
QY 61 SPPSGGVPPGGLPAVALYNSTRDVRVAGESVEPEPEADYAKVTRVLAVESGNOI 120
D 61 SPPSGGVPPGGLPAVALYNSTRDVRVAGESVEPEPEADYAKVTRVLAVETINEI 120
QY 121 YDKEFGTHSLYMLFNTSELREAVPEVLLSRAELRL-RLKLVEQVHVELYOKYSNDSW 179
D 121 YDKEFGTHSLYMLFNTSELREAVPEVLLSRAELRLRLKLVEQVHVELYOKYSNDSW 180
QY 180 RLTSRLRLAPSSPELSDVYGVYKQWLTTRRAIEGFRLSAHSSSDSKNTLHVEINGF 239
D 181 RLTSRLRLAPSSPELSDVYGVYKQWLTTRRAIEGFRLSAHSSSDSKNTLHVEINGF 240
QY 240 NSGRGDLATIGHMNRPFLLMATPLERAQHLS 273
D 241 TTGRGDLATIGHMNRPFLLMATPLERAQHLS 274

RESULT 11
US-09-756-283A-22
; Sequence 22, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
; APPLICANT: Chernajovsky, Yuti
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mIFN -LAP construct
US-09-756-283A-22

Query Match          52.8%; Score 1139; DB 10; Length 447;
Best Local Similarity 87.0%; Pred. No. 7.1e-89;
Matches 228; Conservative 10; Mismatches 18; Indels 6; Gaps 3;
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QY 14 PL-LMLVLTPGRPAAGLSTCKTIDMELVKKRIEAIKGLSKRLASPPSGDVPPGP 72
D 190 PLGLW---AGGSAALSTCKTIDMELVKKRIEAIKGLSKRLASPPSGDVPPGP 245
QY 73 LPEAVIALYNSTRDVRVAGESVEPEPEADYAKVTRVLAVESGNOIYDKFKGPHSLY 132
D 246 LPEAVIALYNSTRDVRVAGESVEPEPEADYAKVTRVLAVETINEIYDKFKGPHSLY 305
QY 133 MLENTSELREAVPEVLLSRAELRL-RLKLVEQVHVELYOKYSNDSWRYSNRLAPSD 191
D 306 MLENTSELREAVPEVLLSRAELRLRLKLVEQVHVELYOKYSNDSWRYSNRLAPSD 365
QY 192 SPEWLSFDVYGVYKQWLTTRRAIEGFRLSAHSSSDSKNTLHVEINGFNSGRGDLATIH 251
D 366 SPEWLSFDVYGVYKQWLTTRRAIEGFRLSAHSSSDSKNTLHVEINGFNSGRGDLATIH 425
QY 252 GMRNPFLLMATPLERAQHLS 273
D 426 GMRNPFLLMATPLERAQHLS 447

RESULT 12
US-09-214-592-32
; Sequence 32, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamashita, Motoo
; APPLICANT: Sato, Chisafumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 32
; LENGTH: 373
; TYPE: PRT
; ORGANISM: chicken
US-09-214-592-32

Query Match          48.5%; Score 1047; DB 9; Length 373;
Best Local Similarity 52.9%; Pred. No. 3.7e-81;
Matches 207; Conservative 52; Mismatches 100; Indels 32; Gaps 8;

QY 30 LSTCKTIMELVKKRIEAIKGLSKRLASPPSGDVPPGGLPAVALYNSTRDVRV 89
D 2 LSTCKTIMELVKKRIEAIKGLSKRLASPPSGDVPPGGLPAVALYNSTRDVRV 61
QY 90 GRS-VEPEPEADYAKVTRVLAVESGNOIYDKFKGPHSLYMLFNTSELREAVPEV 148
D 62 GRARLRPPDPGDEYAKVTRVLAVESGNOIYDKFKGPHSLYMLFNTSELREAVPEV 120
QY 149 LLSRAELRLKLK-----VEQVHVELYOKYSNDSWRYSNRLASPSPEWLSFDVTG 203
D 121 LLSRAELRLKLKAAADSGTDRLRYOGYASWRYLHGKRVKATADEWLSFDVTG 180
QY 204 VQWLTTRRAIEGFRLSAHSSSD---SKDNTLHVEINGFNSGRGDLATIGHMNR--PFL 258
D 181 VQWLTTRRAIEGFRLSAHSSSD---SKDNTLHVEINGFNSGRGDLATIGHMNR--PFL 239
QY 259 LLMATPLERAQHLSRHRRALDNTSYPYDVPIYASLADTNYCF--SSTFKNCVAVQLY 316
D 240 LLMATPLERAQHLSRHRRALDNTSYPYDVPIYASLADTNYCF--SSTFKNCVAVQLY 282
QY 317 IDPKRLGKKWTHPEKGYANFCLGPOPIYWSLDTQYKLYALYQNPASAPCCVPO 376
D 283 IDPKRLGKKWTHPEKGYANFCLGPOPIYWSLDTQYKLYALYQNPASAPCCVPO 342
QY 377 ALEPLPIYVVGKPKVEQLSNMIVSCKCS 407
D 377 ALEPLPIYVVGKPKVEQLSNMIVSCKCS 407
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QY 123 KFKGTPHSLYMTENTSPLEAREVPERVLLSRAELRLRLK--KVEQHVELYOKYGSNDGW- 179
Db 117 -----HEFKFKENASVREYVGNLSLHHHELKMYKKOTDRKNMDORHELFWKYOENGTT 170
QY 180 --RYLSNRLAPSDSPMLSPDYGVVROWL/TRREALIEGFRLSAH---SSDSKDNTLHV 234
Db 171 HSRVLESEKTYITPTVDDDEMSFDYKTVNEWELKRAEENQFGLOPACKCPTPQAKD---I 226
QY 235 EINGENSGRRGDLATIGHM--NRPFLLMATPLERAQHLHSSRRRALDTNSYPYDVPDY 292
Db 227 DIEGF--PALRGDLASLSKENTKPYLMITSHPAERIDVTSSRRKR----- 271
QY 293 ASIALDNTNYCSPSTEKNCCVQOLYIDFRKDLGKWKIHEPKGYHANFCLGPPYIWSLDTQ 352
Db 272 ---GVGOEYCFGNNGPNCVAKPLIYINFRKDLGKWKIHEPKGYEANYCLGNCPIYMSMDTQ 328
QY 353 YSKVYLALYNQHNPGASAPCCVPOALEPLTYVYVYGRKPKVEQLSNMIVRSCKCS 407
Db 329 YSKVLSLYNQNNPGASISPCCVPLLEPLIITYYVGRIAKVEQLSNMIVVRSNCNS 383
```

Search completed: April 15, 2003, 12:04:30
Job time : 134 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:58:28 ; Search time 79 Seconds
(without alignments)
1061.534 Million cell updates/sec

Title: US-10-017-372e-37
Perfect score: 2159
Sequence: 1 MAPSGRLRLPLPLMLLV.....GRRPKVEGLSNMIVRSCKS 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1815.5	84.1	390	6 Q9TUM8	Q9TUM8 equus caball
2	1736.5	80.4	368	11 Q8R4D9	Q8R4D9 sigmodon hi
3	827.5	38.3	412	11 Q91U07	Q91U07 mus musculu
4	825	38.2	382	13 Q9PW49	Q9PW49 morone chry
5	821	38.0	414	11 Q91VP5	Q91VP5 mus musculu
6	806	37.3	382	13 Q93449	Q93449 oncorhynch
7	780	36.1	376	13 Q9PT02	Q9PT02 cyprinus ca
8	760	35.2	399	11 Q9ERB7	Q9ERB7 mesocricetu
9	719.5	33.3	362	11 Q9XK17	Q9XK17 mus musculu
10	691.5	32.0	130	11 Q08714	Q08714 mesocricetu
11	674.5	31.2	124	6 Q95N80	Q95N80 canis famli
12	673.5	31.2	361	13 Q98854	Q98854 cyprinus ca
13	638	29.6	112	6 Q002730	Q002730 oncorhynch
14	600	27.8	255	11 Q921T1	Q921T1 mus musculu
15	584.5	27.1	127	6 Q9TV08	Q9TV08 canis famli
16	561.5	26.0	200	13 Q90YF1	Q90YF1 pleuronecte

17	554	25.7	101	11 Q9R184	Q9R184 meriones un
18	456	21.1	179	13 Q90YF2	Q90YF2 pleuronecte
19	413	19.1	88	13 Q90YF5	Q90YF5 pleuronecte
20	402	18.6	88	13 Q90YF7	Q90YF7 oncorhynch
21	397	18.4	88	13 Q90ZET	Q90ZET acipenser b
22	393	18.2	87	13 Q42306	Q42306 carassius a
23	383	17.7	91	6 Q9MYZ1	Q9MYZ1 capra hircu
24	373	17.3	86	6 Q28241	Q28241 cervus elap
25	371.5	17.2	309	4 Q8WV88	Q8WV88 homo sapien
26	358	16.6	81	6 Q9N1S3	Q9N1S3 capreolus c
27	336.5	15.6	375	13 Q8UWMD	Q8UWMD columba liv
28	321.5	14.9	375	13 Q8UWMD7	Q8UWMD7 colurnix ch
29	321.5	14.9	389	13 Q90YF0	Q90YF0 ictalurus p
30	317	14.7	77	13 Q90YF8	Q90YF8 oncorhynch
31	316.5	14.7	375	6 Q98SP0	Q98SP0 gallus gall
32	313.5	14.5	375	6 Q9GMY7	Q9GMY7 equus cabal
33	313.5	14.5	375	13 Q8UWMD0	Q8UWMD0 anas platyr
34	311.5	14.4	375	13 Q8UWMD9	Q8UWMD9 anser anser
35	306.5	14.2	375	6 Q95V86	Q95V86 macaca fasc
36	302	14.0	50	6 Q28240	Q28240 cervus elap
37	301	13.9	62	13 Q90ZJ7	Q90ZJ7 anguilla an
38	300	13.9	62	13 Q90YF4	Q90YF4 pleuronecte
39	296.5	13.7	375	6 Q8WMS6	Q8WMS6 bos taurus
40	295	13.7	376	13 Q98TB4	Q98TB4 oreochromis
41	294	13.6	376	13 Q90W06	Q90W06 umbrina cir
42	294	13.6	385	13 Q90W05	Q90W05 sparus aura
43	289.5	13.4	373	13 Q90ZD1	Q90ZD1 oncorhynch
44	287.5	13.3	377	13 Q98TB3	Q98TB3 morone chry
45	287	13.3	62	13 Q9DEP5	Q9DEP5 scophthalmu

ALIGNMENTS

RESULT 1

Q9TUM8 ID Q9TUM8 PRELIMINARY; PRT; 390 AA.

AC Q9TUM8; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Transforming growth factor beta 1.
GN TGFBI.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;

RA Nixson A.J., Brower-Toland B.T., Sandell L.J.;
RT "Molecular cloning of equine transforming growth factor beta 1 reveals
RT a divergent nucleotide structure that encodes a novel bioactive
RT peptide among mammalian species."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF175709; AAD49431.1; -.
DR HSSP; P01137; 1KLA.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb.N.
DR InterPro; IPR003911; TGF-TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR01423; TGFbBETA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF-BETA_1; 1.
KW Glycoprotein.

SEQUENCE 390 AA; 43860 MW; 220FE40DFCCA6016 CRC64;

Query Match 84.1%; Score 1815.5; DB 6; Length 390;
Best Local Similarity 85.5%; Pred. No. 3.1e-149;
Matches 348; Conservative 12; Mismatches 30; Indels 17; Gaps 1;


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OY 403 SCSCS 407
DB 408 SCSCS 412

RESULT 4
O9PMA9 PRELIMINARY; PRT: 382 AA.
AC O9PMA9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Transforming growth factor beta precursor.
GN TGF-BETA.
OS Morone chrysops x Morone saxatilis (white bass x striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=45352;
RN [1]
RC SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=KIDNEY;
RX MEDLINE=20394636; PubMed=10938723;
RA Harms C.A., Kennedy-Stoskopf S., Horne W.A., Fuller F.J.,
RA Tompkins W.A.F.;
RT *Cloning and sequencing hybrid striped bass (Morone saxatilis x M.
RT chrysops) transforming growth factor-beta (tgfb-beta), and development
RT of a reverse transcription quantitative competitive polymerase chain
RT reaction (RT-qPCR) assay to measure TGF-beta mRNA of teleost fish";
RL Fish Shellfish Immunol. 10:61-85(2000).
CC -1- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGHER LEVELS FOUND IN MONONUCLEAR CELLS FROM
CC PERIPHERAL BLOOD THAN IN SPLEEN OR ANTERIOR KIDNEY.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC EMBL: AF140363; AAD46997.1; -.
DR HSSB; P01137; IKA4.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF-BETA_1; 1.
DR Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1
FT PROPEP 270
FT CHAIN 271 382 TRANSFORMING GROWTH FACTOR BETA.
FT DISULFID 278 286 BY SIMILARITY.
FT DISULFID 285 348 BY SIMILARITY.
FT DISULFID 314 379 BY SIMILARITY.
FT DISULFID 318 381 BY SIMILARITY.
FT CAROXYHD 347 347 INTERCHAIN (BY SIMILARITY).
FT CAROXYHD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYHD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYHD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYHD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYHD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 237 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 382 AA; 43846 MW; 3124D8C34EA74D72 CRC64;

Query Match 38.2%; Score 825; DB 13; Length 382;
Best Local Similarity 45.3%; Pred. No. 2.8e-63;
Matches 186; Conservative 65; Mismatches 108; Indels 52; Gaps 15;
OY 15 LMLVLVLTGPRPAGLSTCKTIDMELVKKRIEAIKQILSKRL--ASPSCGQDVP 71
DB 6 LMLVVTYVGN-VSGMSTCKTLDEWKKRIEAIKQILSKRLPKPEPDQADEBEI 64
OY 72 PLPEAVLALVNSRDRVAGESVEPE-----PEPADVYAKVTVRVLMWESNQIYDKRG 126
DB 1 PLPEAVLALVNSRDRVAGESVEPE-----PEPADVYAKVTVRVLMWESNQIYDKRG 126

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DB 65 PTP--LILSYNSTKEMLKFOOTEVQTDISTEOEEBEYFAKVLKENMTKNN----- 114
OY 127 TPRSLVWNTSELREAVPEPVLLSRRELRLRLKLV--EQHVELYOKYNSDWRYSLN 184
DB 115 TDYTKKFEFNISELRESVGVRLRLTSABLRLIKTTIYDEQRELYSGL-GDSFRIYAS 173
OY 185 RLAPSDSPEMLSRDVGVYVROWLTRREALIEGF--RLSAHSSSDKMDTL-HVEINGENS 241
DB 174 RFTTNKKDKMWSLSDYKTLQDWLKGTDDEGFLRLFCCECNKVSAGETIFKFGISGIDP 233
OY 242 GRRQDLATIGHMNR--PPLIMATPLERAQHLHS-----SRKRALDTNSYPDVPYASLA 296
DB 234 G-RGDTGPMOLLTQQPPYILTMSIP---QNISSPSYSRKRSTETK----- 275
OY 297 LDNTYCCSTTEKNCVCQLYTDFRKDGKWIHEPKGYHANCPLPCPYIMSLDQYSKV 356
DB 276 --DVCAQGE-TCCVNSLYIDFKDLGKMIHKRTGYINANTCMSCSYIIMNAEKYSOI 331
OY 357 LALYNOHNPASAPCCVPQALEPLPIYVYVGRKPRVQLSNMIVRSCKS 407
DB 332 LALYKHHNPASAPCCVPQALEPLPIYVYVGRKPRVQLSNMIVRSCKS 382

RESULT 5
O91VP5 PRELIMINARY; PRT: 414 AA.
AC O91VP5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Similar to transforming growth factor, beta 2.
GN TGFb2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC EMBL; BC011170; AAH1170.1; -.
DR MGD; MGI:98726; Tgfb2.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR PROSITE; PS00250; TGF-BETA_1; UNKNOWN_1.
DR Growth factor; Mitogen; Glycoprotein.
KV Glycoprotein.
SQ SEQUENCE 414 AA; 47588 MW; DB37A7C38881F286 CRC64;

Query Match 38.0%; Score 821; DB 11; Length 414;
Best Local Similarity 43.3%; Pred. No. 7.1e-63;
Matches 188; Conservative 62; Mismatches 122; Indels 62; Gaps 15;
OY 12 ILPLMLVLTGPRPAGLSTCKTIDMELVKKRIEAIKQILSKRLASPPSGQDVP-P 70
DB 5 VLSTFLHLHV--VALSTSTCTLMDQFMKRIEAIKQILSKRLKLTSPPE--DYPEP 60
OY 71 GLPLPEAVLALVNSRDRVAGESVEPEPE--PEADVYAKVTVRVLM--VESGNOIYD 122
DB 61 DEVPPEVISIYVNSTRLDLOEKASRRAAACERESDEYVAKVYKIDMPSHLSENAIPP 120
OY 123 KFKGPHSLYLMFNTSELREAVPEPVLLSRRELRLRL--KLKV--EQHVELYQ-----K 173
DB 121 TTY-RPYKRIYVFDVSTMEKNSN---LYKAEPRVRLQPKARVAAQRIELVQILSKD 176
OY 174 YNSDWRYSLNRLAPSDSPEMLSRDVGVYVROWLTRREALIEGFRLSAHSS----- 225
DB 177 LNSPTQRYIDSKVVKTRAEGLMSLFDVTDAVQEMLHKDRNLGKISLHCPCTFVPSNN 236

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QY	DB	Query Match	Similarity	Score	DB	Length
QY	DB	18 LVLVTPRPAAGLSTCKTIDMELVYKRRKRIEATRGQILSKRLASPPSGQDVP-PCGLPEPA	42.1%	760;	DB 11;	399;
QY	DB	4 LHLVLP-VALSSTCTIDMDQFMKRRRIEATRGQILSKRLTSPPE--DYPEPDVEPPE	59;	13e-57;	Indels	62;
QY	DB	77 VLALYNSTRD---RVAEASVEPEEP-LEADVYAAKEVRYVLM---VESGNQIYDKFKGTP	128		Gaps	15;
QY	DB	60 VISIYNSTRDLQGEASRRRAACERESDEEYAAKEVYKIDNPSPSENALIPPTFY-RP	118			
QY	DB	129 HSLVLMFTMSLEAREVYPPVLLVRAELRLRY---KLKV-EQHVELYQ---KYSNDWM	179			
QY	DB	119 YFRIYRFVDSMMENKASN---LYKAEFFRYFRLOPNKARVAREQRIEYLQILSKDLTSPQ	175			
QY	DB	180 RYLSNRLIASPDSPEWLSHDVYGVYKQWLTREALEGFRLSAH-----SSDSK	228			
QY	DB	176 RYIDSKVYKTRAEQEWLSPDYDAVHEWLNHDKDRLNGFKISLHCPCTFVPENNIIIPNK	235			
QY	DB	229 DNTLIVE---TAFNPSGRGDLATITGNNR-----PFLLMATPLERAOHLHSSRHRA	279			
QY	DB	236 SEELARRAGIDIGTOSHSSGHOETIKSTRKKNSGKTPHLLMLPBYRLSESQSNRRKR	295			
QY	DB	280 LDTNSYPYDVPDYASLADLTNYCFSSTEKNCCVROLYIDFRKDLGKMTHEPKGYHANC	339			
QY	DB	296 -----ALDAAYCFRRVQDNCCLRPYIDFKRDLGKMTHEPKGYANFC	339			
QY	DB	340 LGRPYIWSLDIYOYSKVLYALNOMHNGASAAPOCQALDEPIYVYVGRKPYVDELSSM	399			
QY	DB	340 AGACEYLMSSDQHKRVLYSLTYNTINPEASAPCCVSHDLEPLITLYIGNTPKIEQLSSM	399			
RESULT 9						
ID	Q99K17	PRELIMINARY:	PRT:	362	AA.	
AC	Q99K17					
DT	01-JUN-2001	(TREMBlrel. 17, Created)				
DT	01-JUN-2001	(TREMBlrel. 17, last sequence update)				
DT	01-JUN-2002	(TREMBlrel. 21, last annotation update)				
DE	Similar to transforming growth factor, beta 3 (fragment).					
GN	TGFβ3.					
OS	Mus musculus (Mouse)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.					
OX	NCBI_TaxID=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Strausberg R.;					
RL	Submitted (Mar-2001) to the EMBL/GenBank/DBJ databases.					
CC	-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.					
DR	EMBL;	BC005513;	AAH0513.1;	--		
DR	HSSP;	P10600;	1TGF.			
DR	MGD;	MGI:98727;	Tgfb3.			
DR	InterPro:	IPR001839;	TGFp.			
DR	InterPro:	IPR001111;	TGFp.N.			
DR	InterPro:	IPR003911;	TGFp.TGfb.			
DR	Pfam;	PF00019;	TGF-beta; 1.			
DR	PRINTS;	PR01423;	TGFBETA.			
DR	ProDom;	PD000357;	TGFp; 1.			
DR	SMART;	SM00204;	TGFB; 1.			
DR	PROSITE;	PS00250;	TGF_BETA_1; 1.			
KW	Glycoprotein.					
FT	NON_TER	1				
FT	NON_TER	399				
SO	SEQUENCE	399	AA;	46078	MM;	AGF8B65EAFD5148 CRC64;

	-1	FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
	-1	SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
DR	EMBL:	X60296; CAA42838.1;..
DR	HSSP:	P01137; IKLA.
DR	InterPro:	IPIR001839; TGFb.
DR	Pfam:	PF000019; TGF-beta; 1.
DR	Prodom:	PD000357; TGFb; 1.
DR	SMART:	SM00204; TGFb; 1.
DR	PROSITE:	PS00250; TGF-BETA_1; 1.
KM	Growth factor:	Mitogen; Glycoprotein.
FT	NON_TER	1
FT	PROPEP	<1
FT	CHAIN	19
FT	DISULFD	25
FT	DISULFD	33
FT	DISULFD	66
FT	DISULFD	95
FT	CONFLICT	93
SO	SEQUENCE	130 AA; 14997 MW; 8B41DD6CF9CCA77 CRC64;
Query Match		32.0%; Score 691.5; DB 11; Length 130;
Best Local Similarity		86.4%; Fred. No. 2.4e-52;
Matches 127; Conservative		0; Mismatches 3; Indels 17; Gaps 1,
QY	261	MATPLERAQHHTSHRRRLADLTNSYPVUDVASLADLTNYCFSSTENKCCVROLYIDFR 320
Dd	1	MATPLERAHQHQSSHRR-----ALDTNYSFSTENKCVROLYIDFR 43
QY	321	KDLGKKWHEPRGYANFCLGPCPYIMSLDIOYSKVYALYNQHNGBASAPCCVPDALEP 380
Dd	44	KDLGKKWHHEPRGYANFCLGPCPYIMSLDIOYSKVYALYNQHNGBASAGPCVPDALEP 103
QY	381	LPIYYVGKRKPVEQLSNMIVRSCKCS 407
Dd	104	LPIYYVGKRKPVEQLSNMIVRSYKCS 130
RESULT 11		
O95N80	ID	O95N80
AC	PRELIMINARY;	PRT; 124 AA.
DT	01-DEC-2001	(TtEmblrel; 19, Created)
DT	01-DEC-2001	(TtEmblrel; 19, Last sequence update)
DT	01-JUN-2002	(TtEmblrel; 21, Last annotation update)
DE	Transforming growth factor beta 1	(Fragment).
OS	Canis familiaris	(Dog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	
OX	NCBI_TaxId=9615;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Fonfara S., Groene A., Baumgaertner W.;	
RT	"Sequence of canine transforming growth factor beta 1 mRNA in DH82-	
RT	cells."	
RU	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.	
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.	
DR	EMBL:	A6349538; AAK54072.1; ..
DR	InterPro:	IPIR001839; TGFb.
DR	Pfam:	PF000019; TGF-beta; 1.
DR	Prodom:	PD000357; TGFb; 1.
DR	PROSITE:	PS00250; TGF-BETA_1; UNKNOWN_1.
KM	Glycoprotein.	
FT	NON_TER	1
FT	NON_TER	124
SO	SEQUENCE	124 AA; 14329 MW; 21D185218E5556DB CRC64;

Query Match 31.2%: Score 674.5; DB 6; Length 124;
Best Local Similarity 87.2%: Pred. No. 6.6e-51;
Matches 123; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

QY 264 PLERAQHLSRRRALDNTSYPDVADYASLALDNTNCFSTSEKNCVROLXIDFRDL 323
DB 1 PLERAQHLSRRQR-----ADNTNCFSTSEKNCVROLXIDFRDL 43
QY 324 GWKWIHEPKGYHANFCGPGCYIWSLDTQYSKVALYNOHNPASAPCCVQALEPLPI 383
DB 44 GWKWIHEPKGYHANFCGPGCYIWSLDTQYSKVALYNOHNPASAPCCVQALEPLPI 103
QY 384 VYVGRKPKVEQLSNMIVRSC 404
DB 104 VYVGRKPKVEQLSNMIVRSC 124

RESULT 12
098854 PRELIMINARY; PRT; 361 AA.
098854;
DC 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE Transforming growth factor beta 2 (TGF-beta 2) (Fragment).
OS *Cyprinus carpio* (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RX MEDLINE=97354301; PubMed=9210595;
RA Sumathi K., Desai K.V., Kondaliah P.;
RT "Isolation of transforming growth factor-beta2 cDNA from a fish,
Gene 191:103-107(1997)."
RL Gene 191:103-107(1997).
-1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
DEPENDENT T-CELL GROWTH.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: U66874; AAB62983.1; -.
DR HSSP: P08112; 2TGI.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb.N.
DR Pfam: PF00688; TGF-beta.1.
DR Pfam: PF00688; TGFb.propeptide.1.
DR ProDom: PD000357; TGFb.1.
DR SMART: SM00204; TGFb.1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1
FT PROPEP <1 257
FT CHAIN 258 361 TRANSFORMING GROWTH FACTOR BETA 2.
FT DISULFID 264 273 BY SIMILARITY.
FT DISULFID 272 335 BY SIMILARITY.
FT DISULFID 334 334 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 361
SQ SEQUENCE 361 AA; 41931 MW; 949930FA970A3FD3 CRC64;

Query Match 31.2%: Score 673.5; DB 13; Length 361;
Best Local Similarity 40.4%: Pred. No. 3.7e-50;
Matches 155; Conservative 54; Mismatches 116; Indels 59; Gaps 14;

QY 52 QILSKRLASPPSGQVDPGP--LPEAVIALYNSYDRVAGSEVPEPEPE-----ADY 104
DB 1 QILSKRLASPPSGQVDPGP--LPEAVIALYNSYDRVAGSEVPEPEPE-----ADY 57

QY 105 AKQVTRVLM--VESGNOIYDKRGPHSLYMLFNTSELREAVPEVLLSRAELRLRL- 160
DB 58 AKQVTRVLM--VESGNOIYDKRGPHSLYMLFNTSELREAVPEVLLSRAELRLRL- 113
QY 161 --KLKY-EGQVETLYO-----KYSNDSWRYSNRLASDSPEWLSFDTGYVROMLRRE 212
DB 114 NPKARVSEQRILELYQLGHKDLTSPYQYIDSKVVRRTGEWLSFDTGVSEWMLHRD 173
QY 213 ATEGFRLSAHSS-----DSKNTLHVEINGFNSG--RQGLATL----HGMR 255
DB 174 RNNGFISLHCPCTIPVSNYIIPNKSEELERAFADIDSFVAGDLKMKRRHSQS 233
QY 256 PELLNATPLERAQHLSRRRALDNTSYPDVADYASLALDNTNCFSTSEKNCVROL 315
DB 234 PHLLMLPLPSYRLESQHS--HQ-----KRALDAFCFRNYQDNCGLRSL 277
QY 316 YIDFRKDLGWKWIHEPKGYHANFCGPGCYIWSLDTQYSKVALYNOHNPASAPCCVP 375
DB 278 YIDFRKDLGWKWIHEPKGYHANFCGPGCYIWSLDTQYSKVALYNOHNPASAPCCVS 337
QY 376 QALEPLPIVYVGRKPKVEQLSNM 399
DB 338 QALEPLPIVYVGRKPKVEQLSNM 361

RESULT 13
002730 PRELIMINARY; PRT; 112 AA.
002730;
DC 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
GN TGFb1 OR TGF-BETA-1.
OS *Oryctolagus cuniculus* (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Taylor T.K., James E.R., Mcgonigle S., Yoho E.R.;
RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
-1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF000133; AAB53806.1; -.
DR EMBL: AB020217; BAA36950.1; -.
DR HSSP: P01137; 1KLA.
DR InterPro: IPR002400; GF_cysknob.
DR InterPro: IPR001839; TGFb.
DR Pfam: PF00019; TGF-beta.1.
DR PRINTS: PR00438; GF_CYSKNOT.
DR ProDom: PD000357; TGFb.1.
DR SMART: SM00204; TGFb.1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1
FT CHAIN 1 112 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 7 16 BY SIMILARITY.
FT DISULFID 15 78 BY SIMILARITY.
FT DISULFID 44 109 BY SIMILARITY.
FT DISULFID 48 111 BY SIMILARITY.
FT DISULFID 77 77 INTERCHAIN (BY SIMILARITY).
FT CONFLICT 2 3 LD -> FS (IN REF. 2).

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FT CONFLICT 85 92 PULPIYVYV -> ATAHRTTL (IN REF. 2).
SQ SEQUENCE 112 AA: 12795 MW: 53CSB7D6355A63 CRC64;
Query Match 29.6%; Score 638; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 8.4e-48;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 296 ADDTWCFSTERNCCVROLYIDPRKDLGKWKIHEPKGYHANFCLGCPPIYMSLDTQYXK 355
DB 1 ADDTWCFSTERNCCVROLYIDPRKDLGKWKIHEPKGYHANFCLGCPPIYMSLDTQYXK 60
QY 356 VALATYQNHNPAGSAAPCCVQALPEPLIYVYVGRKKPYEQLSNMIVRSCKS 407
DB 61 VALATYQNHNPAGSAAPCCVQALPEPLIYVYVGRKKPYEQLSNMIVRSCKS 112
RESULT 14
ID 0921T1 PRELIMINARY; PRT; 255 AA.
AC 0921T1
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to transforming growth factor, beta 2.
GN TGFb2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI-TaxID:10090;
RN 11
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC 11 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL: BC011055; AAH11055.1; -.
MGD: MGI:96726; Tgfb2.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
SQ SEQUENCE 255 AA: 29087 MW: 94540017F3C5C219 CRC64;
Query Match 27.8%; Score 600; DB 11; Length 255;
Best Local Similarity 44.2%; Pred. No. 5.4e-44;
Matches 119; Conservative 42; Mismatches 68; Indels 40; Gaps 6;
QY 163 KYEQ--HVELYQR--YSNDSWRLYNRLAPSDSPFWLSPDYTGVRQWLTRREALTEGFR 218
DB 3 RVEATHVOQLKSKDLSPQRYIDSKVVKTRAGEWLSFDYDAVOELHHKDRNLGFK 62
QY 219 LSAHSSS-----DSKDNTHVE---INGFNSGRGDLATIHGMNR-----PFL 258
DB 63 ISLHPCPCTFVPSNNYIIPKNSLEAFAGIDGTSTYASGDQKTIKSTRKKTSGKPHL 122
QY 259 LMATPLERAQHLHSSRRRALDINSYRVDVYASLADLTNYCFSTERNCCVROLYID 318
DB 123 LMLLPSTRLSEQSSRRKR-----ALDAAYCFRNVDNCCIRPLIYID 166
QY 319 FRKDLGKWKIHEPKGYHANFCLGCPPIYMSLDTQYXKVALATYQNHNPAGSAAPCCVQAL 378
DB 167 FRKDLGKWKIHEPKGYHANFCLGCPPIYMSLDTQYXKVALATYQNHNPAGSAAPCCVQAL 226
QY 379 EPLPIYVYVGRKKPYEQLSNMIVRSCKS 407
DB 227 EPLPIYVYVGRKKPYEQLSNMIVRSCKS 255
RESULT 15
ID 09TV08 PRELIMINARY; PRT; 127 AA.
AC 09TV08
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Transforming growth factor beta-1 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI-TaxID:9615;
RN 11
RP SEQUENCE FROM N.A.
RA German A.J., Helps C.R., Hall E.J., Day M.J.;
RT "Cloning and sequencing of canine transforming growth factor beta 1
RT mRNA."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF091135; AAD46993.1; -.
DR HSSP: P01137; 1KLA.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00688; TGFb_propeptide; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 127 AA: 14641 MW: D46D24ECA89F58DE CRC64;
Query Match 27.1%; Score 584.5; DB 6; Length 127;
Best Local Similarity 77.8%; Pred. No. 4.4e-43;
Matches 112; Conservative 5; Mismatches 10; Indels 17; Gaps 1;
QY 179 WRYLSNRLAPSDSPFWLSPDYTGVRQWLTRREALTEGFRLSAHSSSDSKDNTHVEING 238
DB 1 WRYLSNRLAPSDSPFWLSPDYTGVRQWLTRREALTEGFRLSAHSSSDSKDNTHVEING 60
QY 239 FNSGRGDLATIHGMNRPELLMATPLERAQHLHSSRRRALDINSYRVDVYASLAD 298
DB 61 FSSRRGDLATIHGMNRPELLMATPLERAQHLHSSRRR-----ALD 103
QY 299 TNYCFSTERNCCVROLYIDPRKD 322
DB 104 TNYCFSTERNCCVROLYIDPRKD 127
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Search completed: April 15, 2003, 12:00:28
Job time : 83 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:58:03 ; Search time 21 Seconds
(without alignments)
803.851 Million cell updates/sec

Title: US-10-017-372E-37

Sequence: 2159
1 MAPSGRLPLPLPLMLLV.....GRPKVEQLSNMIVRSCKCS 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2030.5	94.0	390	1	TGFI_PIG
2	1929.5	89.4	390	1	TGFI_SHEEP
3	1916.5	88.8	390	1	TGFI_HUMAN
4	1914.5	88.7	390	1	TGFI_CERAE
5	1893.5	87.7	390	1	TGFI_CANFA
6	1839.5	85.2	390	1	TGFI_HORSE
7	1835.5	85.0	390	1	TGFI_MOUSE
8	1826.5	84.6	390	1	TGFI_CAVPO
9	1572.5	72.8	315	1	TGFI_BOVIN
10	1572.5	72.8	315	1	TGFI_CHICK
11	1047	48.5	373	1	TGFI_XENLA
12	868.5	40.2	382	1	TGFI_XENLA
13	852.5	39.5	412	1	TGFI_CHICK
14	834	38.6	409	1	TGFI_PIG
15	827.5	38.3	410	1	TGFI_MOUSE
16	826.5	38.3	412	1	TGFI_MOUSE
17	824.5	38.2	414	1	TGFI_HUMAN
18	824	38.2	414	1	TGFI_HUMAN
19	809	37.5	414	1	TGFI_HUMAN
20	808.5	37.4	413	1	TGFI_XENLA
21	808	37.4	412	1	TGFI_CHICK
22	805	37.3	445	1	TGFI_PIG
23	805	37.3	442	1	TGFI_RAT
24	482	22.3	112	1	TGFI_BOVIN
25	323.5	15.0	375	1	GDF8_MEIGA
26	321.5	14.9	375	1	GDF8_CHICK
27	311.5	14.4	375	1	GDF8_PIG
28	310.5	14.4	375	1	GDF8_PAPHA
29	308.5	14.3	376	1	GDF8_RAT
30	307.5	14.2	376	1	GDF8_HUMAN
31	306.5	14.2	376	1	GDF8_MOUSE
32	305.5	14.2	375	1	GDF8_SHEEP
33	300	13.9	405	1	GDF8_MOUSE

34	300	13.9	407	1	GDF8_HUMAN	O95390 homo sapien
35	296.5	13.7	375	1	GDF8_BOVIN	O18836 bos taurus
36	280.5	13.0	374	1	GDF8_BRARE	O42222 brachydanio
37	278.5	12.9	345	1	GDF8_RAT	O92217 ratius norv
38	275	12.7	425	1	IHBA_SHEEP	P43032 ovis aries
39	272.5	12.6	424	1	IHBA_PIG	P03970 sus scrofa
40	270.5	12.5	424	1	IHBA_MOUSE	O04958 mus musculu
41	270.5	12.5	424	1	IHBA_RAT	P18331 ratius norv
42	270	12.5	425	1	IHBA_BOVIN	P07995 bos taurus
43	269.5	12.5	426	1	IHBA_HORSE	P55102 equus cabal
44	268.5	12.4	426	1	IHBA_HUMAN	P08476 homo sapien
45	265.5	12.3	424	1	IHBA_CHICK	P27092 gallus gall

ALIGNMENTS

RESULT 1
TGFI_PIG STANDARD; PRT; 390 AA.
AC P07200: P08832:
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN TGFB1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=87174844; PubMed=3470708;
RA Derynck R., Rhee L.;
RL "Sequence of the porcine transforming growth factor-beta precursor."; Nucleic Acids Res. 15:3187-3187(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Miniature swine;
RX MEDLINE=89054010; PubMed=2461367;
RA Kondalajah P., van Obberghen-Schilling E., Ludwig R.L., Dhar R., Sporn M.B., Roberts A.B.;
RT "cDNA cloning of porcine transforming growth factor-beta 1 mRNAs. Evidence for alternate splicing and polyadenylation." J. Biol. Chem. 263:18313-18317(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88335639; PubMed=3166520;
RA Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
RT "Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-beta 1)."; Nucleic Acids Res. 16:8730-8730(1988).
RN [4]
RP SHOWS THAT REF. 3 SEQUENCE IS FROM PIG.
RX Jakowlew S.B.;
RL Unpublished observations (MAR-1996).
RN [5]
RP SEQUENCE OF 279-322.
RX MEDLINE=87102890; PubMed=2879635;
RA Cheliefz S., Weatherbee J.A., Tsang M.L.S., Anderson J.K., Mole J.E., Lucas R., Massague J.;
RT "The transforming growth factor-beta system, a complex pattern of cross-reactive ligands and receptors." Cell 48:409-415(1987).
RL Cell 48:409-415(1987).
-I- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
-I- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
-I- SUBCELLULAR LOCATION: Secreted.


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FT DISULFID 285 294 BY SIMILARITY.
FT DISULFID 293 356 BY SIMILARITY.
FT DISULFID 322 387 BY SIMILARITY.
FT DISULFID 326 389 BY SIMILARITY.
FT DISULFID 355 355 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 244 246 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 390 AA: 44291 MW: 10247299484DOE57 CMC64;

Query Match 89.4%; Score 1929.5; DB 1; Length 390;
Best Local Similarity 89.7%; Pred. No. 4,1e-147;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

OY 1 MAVSGRLPLPLPLPLMLVLTGPGPAAGLSTCKTIDMELVKKRIEATRGILSKRLA 60
DB 1 MPFGRLPLPLPLPLMLVLTGPGPAAGLSTCKTIDMELVKKRIEATRGILSKRLA 60
OY 61 SPSQGVPPPLPEAVLALYNSTRDRVAGSEVPEPEADYKAYEYTVLAVESGNCI 120
DB 61 SPSQGVPPPLPEAVLALYNSTRDRVAGSEVPEPEADYKAYEYTVLAVESGNCI 120
OY 121 YDKRKGPHSLYMDLNTSELREAVPEVLLSRALRLRLKLVEQHWELYKYSNDSWR 180
DB 121 YDKRKGPHSLYMDLNTSELREAVPEVLLSRALRLRLKLVEQHWELYKYSNDSWR 180
OY 121 YDKMKSSHSIYFEFNSELREAVPEVLLSRADYRLRLKLVEQHWELYKYSNDSWR 180
DB 121 YDKMKSSHSIYFEFNSELREAVPEVLLSRADYRLRLKLVEQHWELYKYSNDSWR 180
OY 181 YLSNRLAPSSPEWLSVDYGVVQWITRREATGFRLSAHSSDSKDNTHVLENGFN 240
DB 181 YLSNRLAPSSPEWLSVDYGVVQWITRREATGFRLSAHSSDSKDNTHVLENGFN 240
OY 181 YLSNRLAPSSPEWLSVDYGVVQWITRREATGFRLSAHSSDSKDNTHVLENGFN 240
DB 181 YLSNRLAPSSPEWLSVDYGVVQWITRREATGFRLSAHSSDSKDNTHVLENGFN 240
OY 241 SGRGDLATLIGMNRPFLLMATPLERAOHLHSRRRLADNSPYDVPDVALADLN 300
DB 241 SGRGDLATLIGMNRPFLLMATPLERAOHLHSRRRLADNSPYDVPDVALADLN 300
OY 241 SGRGDLATLIGMNRPFLLMATPLERAOHLHSRRRLADNSPYDVPDVALADLN 300
DB 241 SGRGDLATLIGMNRPFLLMATPLERAOHLHSRRRLADNSPYDVPDVALADLN 300
OY 301 YCESSTEKNCCVROLYIDFRKDLGKWKIHPEKGYANFCLGCPYIWSIDTOYSKYLALY 360
DB 301 YCESSTEKNCCVROLYIDFRKDLGKWKIHPEKGYANFCLGCPYIWSIDTOYSKYLALY 360
OY 284 YCESSTEKNCCVROLYIDFRKDLGKWKIHPEKGYANFCLGCPYIWSIDTOYSKYLALY 343
DB 284 YCESSTEKNCCVROLYIDFRKDLGKWKIHPEKGYANFCLGCPYIWSIDTOYSKYLALY 343
OY 361 NQHPGASAPCCVQALPEPLPIYVYVGRKPKVPEOLSNMIVSCSCS 407
DB 361 NQHPGASAPCCVQALPEPLPIYVYVGRKPKVPEOLSNMIVSCSCS 407
OY 344 NQHPGASAPCCVQALPEPLPIYVYVGRKPKVPEOLSNMIVSCSCS 390
DB 344 NQHPGASAPCCVQALPEPLPIYVYVGRKPKVPEOLSNMIVSCSCS 390

RESULT 3
TGFI_HUMAN STANDARD; PRT; 390 AA.
AC P01137; Q9UCG4;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN TGFBI OR TGFBI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid:9606;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE-85296301; PubMed-3861940;
RA Derynck R., Jarrett J.A., Chen E.Y., van Tilburg A.,
RA Assoulin R.K., Roberts A.B., Sporn M.B., Goeddel D.V.;
RA "Human transforming growth factor-beta complementary DNA sequence and
RT expression in normal and transformed cells.";
RL Nature 316:701-705(1985).
[3]

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RP SEQUENCE FROM N.A.
RC TISSUE-Duodenal, and Eye;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE OF 279-390 FROM N.A.
RC TISSUE-Carcinoma;
RA Urushizaki Y., Nitsui Y., Terui T., Koshida Y., Mahara K., Kohgo Y.,
RA Urushizaki I., Takahashi Y., Ito H.;
RT "Cloning and expression of the gene for human transforming growth
RT factor-beta in Escherichia coli.";
RL Tumor Res. 22:41-55(1987).
[5]
RP SEQUENCE OF 279-329.
RC TISSUE-Bladder carcinoma;
RX MEDLINE-93229900; PubMed-8471846;
RA Boudrel L., Lin C.-H., Lauren S.L., Elmore R.H., Sugerman B.J.,
RA Hu S., Westcott K.R.;
RT "Recombinant human transforming growth factor-beta 1: expression by
RT Chinese hamster ovary cells, isolation, and characterization.";
RL Protein Expr. Purif. 4:130-140(1993).
[6]
RP SEQUENCE OF 279-301.
RX MEDLINE-85131019; PubMed-2982829;
RA Massague J., Like B.;
RT "Cellular receptors for type beta transforming growth factor. Ligand
RT binding and affinity labeling in human and rodent cell lines.";
RL J. Biol. Chem. 260:2636-2645(1985).
[7]
RP STRUCTURE BY NMR OF 279-390.
RX MEDLINE-93144319; PubMed-8424942;
RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA Torchia D.A.;
RT "Transforming growth factor beta 1: NMR signal assignments of the
RT recombinant protein expressed and isotopically enriched using Chinese
RT hamster ovary cells.";
RL Biochemistry 32:1152-1163(1993).
[8]
RP STRUCTURE BY NMR OF 279-390.
RX MEDLINE-93144320; PubMed-8424943;
RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA Torchia D.A.;
RT "Transforming growth factor beta 1: secondary structure as determined
RT by heteronuclear magnetic resonance spectroscopy.";
RL Biochemistry 32:1164-1171(1993).
[9]
RP STRUCTURE BY NMR OF 279-390.
RX MEDLINE-96266150; PubMed-8679613;
RA Hnick A.P., Archer S.J., Qian S.W., Roberts A.B., Sporn M.B.,
RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA Torchia D.A.;
RT "Transforming growth factor beta 1: three-dimensional structure in
RT solution and comparison with the X-ray structure of transforming
RT growth factor beta 2.";
RL Biochemistry 35:8517-8534(1996).
-1- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION,
CC DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
CC CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE
CC SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
CC POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SITE 244 246 CELL ATTACHMENT SITE (POTENTIAL).
 SQ SEQUENCE 390 AA: 44356 MW: DFF63E2B8B44320E CMC64;

Query Match 88.7%; Score 1914.5; DB 1; Length 390;
 Best Local Similarity 89.4%; Pred. No. 6.5e-146;
 Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;

QY 1 MAPSGGLRLPLPLPLMLVLTTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 DB 1 MPBSGLRLPLPLPLMLVLTTPSRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 QY 61 SPSQGVPPGPEPLPEAVLALYNSTRDVRAGESVEPEPEADYAKVETRYLVAVESGNOI 120
 DB 61 SPSQGVPPGPEPLPEAVLALYNSTRDVRAGESVEPEPEADYAKVETRYLVAVESGNOI 120
 QY 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRALRLRLKLVQOHVELYOKYSNDSNR 180
 DB 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRALRLRLKLVQOHVELYOKYSNDSNR 180
 QY 181 YLSRRLAPSDPEMLSPDVTGVVROWLITRREALTGFRLSAHSSSDSKONTLHVEINGFN 240
 DB 181 YLSRRLAPSDPEMLSPDVTGVVROWLITRREALTGFRLSAHSSSDSKONTLHVEINGFN 240
 QY 241 SGRSGDLATIGHMNRPEFLLMATPLERAQHLHSSRRRALDNTSYPDVYASLALDTN 300
 DB 241 TGRGDLATIGHMNRPEFLLMATPLERAQHLHSSRRRALDNTSYPDVYASLALDTN 300
 QY 301 YCSSTERNCCVROLYIDFRKDLGKWKIHEPKGYANFLGCPPIYWSLDTQYSKYLALY 360
 DB 284 YCSSTERNCCVROLYIDFRKDLGKWKIHEPKGYANFLGCPPIYWSLDTQYSKYLALY 343
 QY 361 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVSCSCS 407
 DB 344 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVSCSCS 390

RESULT 5
 TGF1_CANFA STANDARD: PRT: 390 AA.

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN TGFBI.
 OS Canis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 ON NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Jugular vein endothelial;
 RX MEDLINE=95237630; PubMed=7721110;
 RA Manning A.M., Auchampach J.A., Drono R.F., Slightom J.L.;
 RT "Cloning of a canine cDNA homologous to the human transforming growth
 factor-beta 1-encoding gene.";
 RL Gene 155:307-308(1995).
 CC -1- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
 PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
 TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
 CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
 ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
 CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -1- SUBUNIT: HOMODIMER. DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).

DR EMBL: I34956; AAA51458.1; -
 DR HSSP: P01137; IRLA
 DR InterPro: IPR002400; GF_cysknob.
 DR InterPro: IPR003911; TGF_TGFB.
 DR InterPro: IPR001839; TGFB.
 DR InterPro: IPR001111; TGFB.N.
 DR Pfam: PR00019; TGF-beta; 1.
 DR Pfam: PR00688; TGFB_propeptide; 1.
 DR PRINTS: PR00438; GFCISKNOT.
 DR PRINTS: PR01423; TGFBETA.
 DR ProDom: PD000357; TGFB.
 DR SMART: SM00204; TGFB; 1.
 DR ProSite: PS00250; TGF_BETA1; 1.
 KW Growth factor; Mitogen; Glycoprotein; Signal.
 FT SIGNAL. 1 23
 FT PROPEP 24 278
 FT CHAIN 279 390
 FT DISULFID 285 294
 FT DISULFID 293 356
 FT DISULFID 322 387
 FT DISULFID 326 389
 FT DISULFID 355 355
 FT CARBOHYD 82 82
 FT CARBOHYD 136 136
 FT CARBOHYD 176 176
 FT SITE 244 246
 SQ SEQUENCE 390 AA: 44185 MW: E4780E8B7B590E CMC64;

Query Match 87.7%; Score 1893.5; DB 1; Length 390;
 Best Local Similarity 88.7%; Pred. No. 3.1e-144;
 Matches 361; Conservative 12; Mismatches 17; Indels 17; Gaps 1;

QY 1 MAPSGGLRLPLPLPLMLVLTTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 DB 1 MPBSGLRLPLPLPLMLVLTTPSRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 QY 61 SPSQGVPPGPEPLPEAVLALYNSTRDVRAGESVEPEPEADYAKVETRYLVAVESGNOI 120
 DB 61 SPSQGVPPGPEPLPEAVLALYNSTRDVRAGESVEPEPEADYAKVETRYLVAVESGNOI 120
 QY 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRALRLRLKLVQOHVELYOKYSNDSNR 180
 DB 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRALRLRLKLVQOHVELYOKYSNDSNR 180
 QY 121 YEKVKKSPHSIYMLFNTSELREAVPEVLLSRALRLRLKLVQOHVELYOKYSNDSNR 180
 DB 181 YLSRRLAPSDPEMLSPDVTGVVROWLITRREALTGFRLSAHSSSDSKONTLHVEINGFN 240
 DB 181 YLSRRLAPSDPEMLSPDVTGVVROWLITRREALTGFRLSAHSSSDSKONTLHVEINGFN 240
 QY 241 SGRSGDLATIGHMNRPEFLLMATPLERAQHLHSSRRRALDNTSYPDVYASLALDTN 300
 DB 241 SGRSGDLATIGHMNRPEFLLMATPLERAQHLHSSRRRALDNTSYPDVYASLALDTN 300
 QY 301 YCSSTERNCCVROLYIDFRKDLGKWKIHEPKGYANFLGCPPIYWSLDTQYSKYLALY 360
 DB 284 YCSSTERNCCVROLYIDFRKDLGKWKIHEPKGYANFLGCPPIYWSLDTQYSKYLALY 343
 QY 361 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVSCSCS 407
 DB 344 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVSCSCS 390
 RESULT 6
 TGF1_HORSE STANDARD: PRT: 390 AA.
 ID TGF1_HORSE
 AC 019011;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN TGFBI.

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OY 181 YLSNRLLAPSDSPMLSDFTGVVROWMLTRREAIIBGFRLSANSSSDSKONTLHVEINGFN 240
Db 181 YLSNRLLTPSDSPMLSEFDYGVVROWMSOGAMEGEFRLSANSCSDSKONTLRVINGEFS 240
OY 241 SGRGRDLATIHGMRRPEFLMATPLERQHLHSRRRLALDNTSYDPYDVAYSLADTN 300
Db 241 SSRGRDLATIIDGMRRPEFLMATPLERQQLHSSRRR-----ALDTN 283
OY 301 YCFSSSTEKNCCVROLYIDFRKDLGWKMIHEPKGYHANFCLGPCPYTWSLDTQYSKVLALY 360
Db 284 YCFSSSTEKNCCVROLYIDFRKDLGWKMIHEPKGYHANFCLGPCPYTWSLDTQYSKVLALY 343
OY 361 NONNPGASAPCCVPOALEPLPIYTVYGRKPKVEOLSNMIVRSCKS 407
Db 344 NONNPGASAPCCVPOYLEPLPIYTVYGRKPKVEOLSNMIVRSCKS 390

RESULT 7
TGFL_MOUSE
ID TGFL_MOUSE STANDARD; PRT: 390 AA.
AC P04202;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN TGFB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86168129; PubMed=3007454;
RA Derynck R., Jarrett J.A., Chen E.Y., Goeddel D.V.;
RT "The murine transforming growth factor-beta precursor.";
RL J. Biol. Chem. 261:4377-4379(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C;
RC MEDLINE=96096545; PubMed=8522200;
RA Guron C., Sudarshan C., Raghow R.;
RT "Molecular organization of the gene encoding murine transforming
growth factor beta 1.";
RL Gene 165:325-326(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6, and NOD/LT; TISSUE=Spleen;
RC Polrot L., Benoist C., Mathis D.;
RT "Transforming growth factor-beta 1 sequence and expression: no
difference between NOD/Lt and C57BL/6 mouse strains.";
RL Submitted (Aug-6-1998) to the EMBL/GenBank/DBJ databases.
CC -i- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -i- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -i- SUBCELLULAR LOCATION: Secreted.
CC -i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M13177; AAA0423.1; -
DR EMBL: L42462; AAB00138.1; -
DR EMBL: L42456; AAB00138.1; JOINED.
RR EMBL: L42457; AAB00138.1; JOINED.

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EMBL: L42458; AAB00138.1; JOINED.
 DR EMBL: L42459; AAB00138.1; JOINED.
 DR EMBL: L42460; AAB00138.1; JOINED.
 DR EMBL: L42461; AAB00138.1; JOINED.
 DR EMBL: A009862; CAA08900.1; -.
 DR PIR: A01396; MFS2.
 DR HSSP: P01137; 1KLA.
 DR MGD: MGI:98725; Tgfb1.
 DR InterPro: IPR002400; GF_cyskn0t.
 DR InterPro: IPR003911; GF_TGFB.
 DR InterPro: IPR001839; TGFB.
 DR InterPro: IPR001111; TGFB.N.
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGFB_propeptide; 1.
 DR PRINTS: PR00438; GFCYSKN0T.
 DR PRINTS: PR01423; TGFBETA.
 DR PRODOM: PD000357; TGFB; 1.
 DR SMART: SM00204; TGFB; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 DR Growth factor; Mitogen; Glycoprotein; signal.
 KW SIGNAL 1
 FT PROPEP 24 278
 FT CHAIN 279 390
 FT DISULFID 285 294
 FT DISULFID 293 356
 FT DISULFID 322 387
 FT DISULFID 326 389
 FT DISULFID 355 355
 FT CARBOHYD 82 82
 FT CARBOHYD 136 136
 FT CARBOHYD 176 176
 FT SITE 244 246
 SO SEQUENCE 390 AA; 44310 MW; 4381A51B71D689E CRC64;
 Query Match 85.0%; Score 1835.5; DB 1; Length 390;
 Best Local Similarity 85.0%; Pred. No. 1.4e-139;
 Matches 346; Conservative 15; Mismatches 29; Indels 17; Gaps 1;

1 MAPSGRLPLPLPLMLVLVTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 DB 1 MPBSGLRLPLPLPLMLVLVTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 QY 61 SPSGQGVPPGRLPEAVLALYNSTRDVAGSEVEPEPEADYAKETRYLVAVESGNOI 120
 DB 61 SPSGQGVPPGRLPEAVLALYNSTRDVAGSEADPEPEADYAKETRYLVAVDRNNAI 120
 QY 121 YDKKRGPHSLYMLFNTSELREAVPEPYLSRAELRLRLKLYQOHVLYKYSDSKR 180
 DB 121 YDKKRGPHSLYMLFNTSELREAVPEPYLSRAELRLRLKLYQOHVLYKYSDSKR 180
 QY 121 YDKKRGPHSLYMLFNTSELREAVPEPYLSRAELRLRLKLYQOHVLYKYSDSKR 180
 DB 121 YDKKRGPHSLYMLFNTSELREAVPEPYLSRAELRLRLKLYQOHVLYKYSDSKR 180
 QY 181 YLSRRLAPSDSPMLSPDVTGVVROWLTRREALIEGFRLSAHSSSDSKONTLHVEINGFN 240
 DB 181 YLSRRLAPSDSPMLSPDVTGVVROWLTRREALIEGFRLSAHSSSDSKONTLHVEINGFN 240
 QY 241 SGRGGDLATTHGNRRPELLMATPLERAQHLHSSRRRALDTSYVDVAYASALDNT 300
 DB 241 SGRGGDLATTHGNRRPELLMATPLERAQHLHSSRRRALDTSYVDVAYASALDNT 300
 QY 241 PKRGDGLTIDHMRPFLLMATPLERAQHLHSSRRRALDTSYVDVAYASALDNT 300
 DB 241 PKRGDGLTIDHMRPFLLMATPLERAQHLHSSRRRALDTSYVDVAYASALDNT 300
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 DB 301 YCFSTENKCCVROLYIDFKDGLGKWIHERKGYHANCLGCPYIWSIDTQYSKYLALY 360
 QY 361 NQHPGASAPCVPAOLEPLPIYVYVGRPKVEQLSNMIVSCSKCS 407
 DB 361 NQHPGASAPCVPAOLEPLPIYVYVGRPKVEQLSNMIVSCSKCS 407
 QY 344 NQHPGASAPCVPAOLEPLPIYVYVGRPKVEQLSNMIVSCSKCS 390
 DB 344 NQHPGASAPCVPAOLEPLPIYVYVGRPKVEQLSNMIVSCSKCS 390
 RESULT 8
 TGF_L_RAT STANDARD: PRT: 390 AA.
 AC P17246;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN TGFb1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Heart;
 RX MEDLINE=90272425; PubMed=2349108;
 RA Qian S.W., Kondalish P., Roberts A.B., Sporn M.B.;
 RT cDNA cloning by PCR of rat transforming growth factor beta-1.;
 RL Nucleic Acids Res. 18:3059-3059(1990).
 CC -1- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
 CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
 CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
 CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 DR EMBL: X52498; CAA36741.1; -.
 DR PIR: S10219; S10219.
 DR HSSP: P01137; 1KLA.
 DR InterPro: IPR002400; GF_cyskn0t.
 DR InterPro: IPR003911; TGF_TGFB.
 DR InterPro: IPR001839; TGFB.
 DR InterPro: IPR001111; TGFB.N.
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGFB_propeptide; 1.
 DR PRINTS: PR00438; GFCYSKN0T.
 DR PRINTS: PR01423; TGFBETA.
 DR PRODOM: PD000357; TGFB; 1.
 DR SMART: SM00204; TGFB; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 DR Growth factor; Mitogen; Glycoprotein; signal.
 KW SIGNAL 1
 FT PROPEP 24 278
 FT CHAIN 279 390
 FT DISULFID 285 294
 FT DISULFID 293 356
 FT DISULFID 322 387
 FT DISULFID 326 389
 FT DISULFID 355 355
 FT CARBOHYD 82 82
 FT CARBOHYD 136 136
 FT CARBOHYD 176 176
 FT SITE 244 246
 SO SEQUENCE 390 AA; 44329 MW; 5E21108ED50D853C CRC64;

Query Match 85.0%; Score 1835.5; DB 1; Length 390;
 Best Local Similarity 85.0%; Pred. No. 1.4e-139;
 Matches 346; Conservative 14; Mismatches 30; Indels 17; Gaps 1;

1 MAPSGRLPLPLPLMLVLVTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 DB 1 MPBSGLRLPLPLPLMLVLVTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 QY 61 SPSGQGVPPGRLPEAVLALYNSTRDVAGSEVEPEPEADYAKETRYLVAVESGNOI 120
 DB 61 SPSGQGVPPGRLPEAVLALYNSTRDVAGSEADPEPEADYAKETRYLVAVDRNNAI 120

QY 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVKEQHVLEYOKYSNDSWR 180
 DB 121 YDKRKDITHSTYMFNTSDIRAEVPEPILLSRAELRLQKFSVEQHVLEYOKYSNDSWR 180
 QY 181 YLSNRLAPSDPEWLSFDVYGVVROWLTRRAELIEGFRLSAHSSSDKNTLHVEINGFN 240
 DB 181 YLSNRLAPSDPEWLSFDVYGVVROWLTRRAELIEGFRLSAHSSSDKNTLHVEINGFN 240
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 DB 241 PKRGDGLTHDMNRPFLLMATPLERAOHLHSSRRRLADTNSYPYDVVDYASLADTN 300
 QY 301 YCFSTERNKCCVROLYIDPRKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVYALY 360
 DB 301 YCFSTERNKCCVROLYIDPRKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVYALY 360
 QY 361 NOHNPGASAPCCVPOALEPLPIYVYVGRKPKVEOLSNMIVRSCKS 407
 DB 361 NOHNPGASAPCCVPOALEPLPIYVYVGRKPKVEOLSNMIVRSCKS 407
 QY 344 NOHNPGASAPCCVPOALEPLPIYVYVGRKPKVEOLSNMIVRSCKS 390
 DB 344 NOHNPGASAPCCVPOALEPLPIYVYVGRKPKVEOLSNMIVRSCKS 390

RESULT 9

TGF1_CAVPO STANDARD; PRT: 390 AA.
 AC 09216; Q9Q2B3; Q9R148;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN TGFBI.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 MX Mammalia; Eutheria; Rodentia; Hystriolognathi; Cavidae; Cavia.
 NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hartley;
 RT Jeevan A., McMurray D.N., Yoshimura T.;
 RT "Guinea pig transforming growth factor-beta in peritoneal exudates
 RT after BCG vaccination.";
 RT Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 265-382 FROM N.A.
 RX MEDLINE=9914670; PubMed=10025978;
 RX Scarotza A.M., Ramsingh A.I., Micher V., Micher K.;
 RT "Spontaneous cytokine gene expression in normal guinea pig blood and
 RT tissues.";
 RT Cytokine 10:851-859(1998).
 RN [3]
 RP SEQUENCE OF 279-371 FROM N.A.
 RC STRAIN=Hartley; TISSUE=Trachea;
 RA Morishima Y., Uchida Y., Nomura A., Ishii Y., Sakamoto T.,
 RA Sekizawa K.;
 RT "Guinea-pig transforming growth factor-beta expression in injured
 RT tracheal epithelium.";
 RT Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
 RL -1- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION,
 RL DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
 RL CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE
 RL SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE
 RL ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
 RL POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 RL -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 RL -1- SUBCELLULAR LOCATION: Secreted.
 RL -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: AF191297; AAF02780.1; -
 DR EMBL: AF097509; AAC83807.1; -
 DR EMBL: AF169347; AAD49347.1; -
 DR HSSP: P01137; IKLA.
 DR InterPro: IPR003911; TGF_TGFB.
 DR InterPro: IPR001839; TGFB.
 DR InterPro: IPR001111; TGFB_N.
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGFB_propeptide; 1.
 DR PRINTS: PR01423; TGFbeta.
 DR ProDom: PD000357; TGFB; 1.
 DR SMART: SM00204; TGFB; 1.
 DR PROSITE: PS00250; TGF-BETA_1; 1.
 KW Growth factor; Mitogen; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT PROPEP 25 278
 FT CHAIN 279 390
 FT DISULFD 285 294
 FT DISULFD 293 356
 FT DISULFD 322 387
 FT DISULFD 326 389
 FT DISULFD 355 355
 FT CARBOHYD 82 82
 FT CARBOHYD 136 136
 FT CARBOHYD 176 176
 FT SITE 244 246
 FT CONFLICT 279 279
 FT CONFLICT 286 286
 FT CONFLICT 309 309
 FT CONFLICT 322 322
 FT CONFLICT 350 350
 SQ SEQUENCE 390 AA: 44328 MW: 1539F849BA0C0F1 CRC64;
 Query Match 84.6%; Score 1826.5; DB 1; Length 390;
 Best Local Similarity 84.8%; Pred. No. 7.3e-139;
 Matches 345; Conservative 15; Mismatches 30; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLPVGRPAAGISCTKIDMELVKRRIRAIKQLISKRLA 60
 DB 1 MPPSRRLPLPLPLMLVLPVGRPAAGISCTKIDMELVKRRIRAIKQLISKRLA 60
 QY 61 SPSSGDVPPGPLPEAVLALYNSTRDVAGESEYEPEPEADYAKETVRLWESGNOI 120
 DB 61 SPSSGDVPPGPLPEAVLALYNSTRDVAGESEYEPEPEADYAKETVRLWDSNGINI 120
 QY 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVKEQHVLEYOKYSNDSWR 180
 DB 121 YKSIETVAHSIYMFNTSELREAVPDLILSRAELRQKRLKLVKEQHVLEYOKYSNDSWR 180
 QY 181 YLSNRLAPSDPEWLSFDVYGVVROWLTRRAELIEGFRLSAHSSSDKNTLHVEINGFN 240
 DB 181 YLSNRLAPSDPEWLSFDVYGVVROWLTRRAELIEGFRLSAHSSSDKNTLHVEINGFN 240
 QY 241 SGRGDLATIHGMNRPFLLMATPLERAOHLHSSRRRLADTNSYPYDVVDYASLADTN 300
 DB 241 PKRGDGLTHDMNRPFLLMATPLERAOHLHSSRRRLADTNSYPYDVVDYASLADTN 300
 QY 301 YCFSTERNKCCVROLYIDPRKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVYALY 360
 DB 301 YCFSTERNKCCVROLYIDPRKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVYALY 360
 QY 361 NOHNPGASAPCCVPOALEPLPIYVYVGRKPKVEOLSNMIVRSCKS 407
 DB 361 NOHNPGASAPCCVPOALEPLPIYVYVGRKPKVEOLSNMIVRSCKS 407
 QY 344 NOHNPGASAPCCVPOALEPLPIYVYVGRKPKVEOLSNMIVRSCKS 390
 DB 344 NOHNPGASAPCCVPOALEPLPIYVYVGRKPKVEOLSNMIVRSCKS 390

RESULT 10

TGF1_BOVIN STANDARD; PRT: 315 AA.
 AC P18341;
 DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1) (Fragment).
 OS TGFBI.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91042552; PubMed=3153459;
 RA van Obberghen-Schilling E., Kondaliah P., Ludwig R.L., Sporn M.B.,
 RA Baker C.C.;
 RT "Complementary deoxyribonucleic acid cloning of bovine transforming
 RT growth factor-beta 1";
 RL Mol. Endocrinol. 1:693-698(1987).
 RN [2]
 RN SUBUNITS.
 RC TISSUE=Bone;
 RX MEDLINE=92129307; PubMed=1733936;
 RA Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;
 RT "Purification and characterization of transforming growth factor-beta
 RT 2.3 and -beta 1.2 heterodimers from bovine bone.";
 RL J. Biol. Chem. 267:2325-2328(1992).
 CC -1- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
 CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
 CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
 CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. HETERODIMERS OF TGF-BETA 1/2
 CC HAVE BEEN FOUND IN BONE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL; M36271; AAA30778.1; -.
 DR PIR; A40057; A40057.
 DR HSP; P01137; 1KLA.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF-BETA_1; 1.
 KW Growth factor; Mitogen; Glycoprotein.
 KM
 FT NON_TER 1
 FT PROPEP 1
 FT CHAIN 203
 FT DISULFID 204 315 TRANSFORMING GROWTH FACTOR BETA 1.
 FT DISULFID 210 219 BY SIMILARITY.
 FT DISULFID 218 281 HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
 FT DISULFID 247 312 BY SIMILARITY.
 FT DISULFID 251 314 BY SIMILARITY.
 FT DISULFID 280 280 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 169 171 CELL ATTACHMENT SITE (POTENTIAL).
 SQ SEQUENCE 315 AA; 36269 MW; C217A23B994E00E CRC64;
 Query Match 72.8%; Score 1572.5; DB 1; Length 315;
 Best Local Similarity 88.9%; Pred. No. 1.2e-118;
 Matches 295; Conservative 9; Mismatches 11; Indels 17; Gaps 1;

DB 1
 1 AILALYNSTRDRVAGSASAEPEPEADYAKVETRYLWVESGNQIYDKRKGTPTSLMLF 135
 QY 136 NTSLEAEAPPEPILSRALRLRLKIKYQHWELYOKYNSDSRWYLSNRLAPSDSPW 195
 DB 61 NTSLEAEAPPEPILSRADRLRLKIKYQHWELYOKYNSDSRWYLSNRLAPSDSPW 120
 QY 196 LSPDYGVVQWLTREAEIGFRLSAHSSDSKDNLTAVEINGNSGRGLATIHGMNR 255
 DB 121 LSPDYGVVQWLTREAEIGFRLSAHSSDSKDNLTAVEINGNSGRGLATIHGMNR 180
 QY 256 PELLMTATPLERAQHLSHRRRALDYNSTPYDVAASALDITNGFSSTEKNCVROL 315
 DB 181 PELLMTATPLERAQHLSHRRRALDYNSTPYDVAASALDITNGFSSTEKNCVROL 223
 QY 316 YDFPRDLGKWKIHEPRGYANFCLGPCPIYWSLDTQYSKVALYNOHNPASAPCCVP 375
 DB 224 YDFPRDLGKWKIHEPRGYANFCLGPCPIYWSLDTQYSKVALYNOHNPASAPCCVP 283
 QY 376 QALEPLPIYVYGRKPKVEQLSNMIVRSCKS 407
 DB 284 QALEPLPIYVYGRKPKVEQLSNMIVRSCKS 315
 RESULT 11
 TGF1_CHICK STANDARD; PRT; 373 AA.
 ID TGF1_CHICK
 AC P09531;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1) (TGF-beta 4)
 DE (Fragment).
 GN TGFBI.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=White leghorn;
 RC MEDLINE=89112198; PubMed=2464131;
 RA Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
 RT "Complementary deoxyribonucleic acid cloning of a messenger
 RT ribonucleic acid encoding transforming growth factor beta 4 from
 RT chicken embryo chondrocytes";
 RL Mol. Endocrinol. 2:1186-1195(1988).
 RN [2]
 RN REVISIONS.
 RX MEDLINE=92357039; PubMed=1333860;
 RA Burt D.W., Jakowlew S.B.;
 RT "Correction: a new interpretation of a chicken transforming growth
 RT factor-beta 4 complementary DNA.";
 RL Mol. Endocrinol. 6:989-992(1992).
 CC -1- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
 CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
 CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
 CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC -----

EMBL; M31160; AAB05637.1; -
 DR PIR; A34941; A34941.
 DR PIR; S03110; S03110.
 DR HSSP; P01137; IKLA.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_beta_1; 1.
 DR Growth factor; Mitogen; Glycoprotein; Signal.
 KM Growth factor; Mitogen; Glycoprotein; Signal.
 FT NON_TER 1
 FT SIGNAL 1
 FT PROPEP 2
 FT CHAIN 259
 FT DISULFID 260
 FT DISULFID 266
 FT DISULFID 275
 FT DISULFID 276
 FT DISULFID 305
 FT DISULFID 309
 FT DISULFID 338
 FT DISULFID 338
 FT CARBOHYD 54
 FT CARBOHYD 109
 FT CARBOHYD 153
 FT CARBOHYD 153
 FT SITE 224
 FT SITE 225
 SQ SEQUENCE 373 AA: 42634 MW: 99035479C8552E5 CRC64;

Query Match
 Best Local Similarity 48.5%; Score 1047; DB 1; Length 373;
 Matches 207; Conservative 52; Mismatches 100; Indels 32; Gaps 8;

30 LSTCKITDMLVKKRIEATRGQLSKRLASPSQGDVPGCPPEALVALYNSTRDVA 89
 2 LSTCKITDMLVKKRIEATRGQLSKRLASPSQGDVPGCPPEALVALYNSTRDVA 89
 90 GES-VEPEPEADYVKEVTRVAVESGNOYOKFKGPHSLVLFNLSLEAREPEV 148
 62 QKRLKRPPEPPEYMAKELKRIMETTWDAEMHMOQSHSIFEFVNSRRARR-GRPT 120
 149 LLSRAELRLRLK-----VEQHEVLYQKYSNDWRVLSNRLASPSPEMLSPDVTGV 203
 121 LLSRAELRLRLKAAADAGTEQRLLEYOGYGNMSWRYLHGHSVATADDEMLSPVDTA 180
 204 VQWMLTRREALIEGFRLSAHSSD---SKDNLHVEINFGNSRRDGLTIHGMR--PEL 258
 181 VQWMLTRREALIEGFRLSAHSSD---SKDNLHVEINFGNSRRDGLTIHGMR--PEL 258
 259 LMATPELERAQHSHSRRAALDNTSYRVDVDAASLADNTYCF--SSTEKNCCVROLY 316
 240 LMATPELERAQHSHSRRAALDNTSYRVDVDAASLADNTYCF--SSTEKNCCVROLY 316
 317 IDERKDLGWKWIHEPKGYHANFCLGCPRYTWSLDTOYSKVALYNQHNPGASAPCCVPQ 376
 283 IDERKDLGWKWIHEPKGYHANFCLGCPRYTWSLDTOYSKVALYNQHNPGASAPCCVPQ 342
 377 ALEPLRVVYVGGKPKYEOLSNMIVRSCKCS 407
 343 TDPLPLIYVGRNVREQLSNMIVRSCKCS 373

RESULT 12
 TGF1_XENLA
 ID TGF1_XENLA STANDARD; PRT; 382 AA.
 DC P16176;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1) (TGF-beta 5).
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 CC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90110090; PubMed=2295601;
 RA Kondalah P., Sands W.J., Smith J.M., Fields A., Roberts A.B.,
 RA Sporn M.B., Melton D.A.;
 RT "Identification of a novel transforming growth factor-beta (TGF-beta
 RT 5) mRNA in Xenopus laevis";
 RL J. Biol. Chem. 265:1089-1093 (1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Vempati U.D., Kondalah P.;
 RL Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: IMPORTANT ROLE IN CERTAIN ASPECTS OF DIFFERENTIATION.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL; J05180; AAA49968.1; -
 DR EMBL; AF009335; AAB64441.1; -
 DR EMBL; AF009331; AAB64441.1; JOINED.
 DR EMBL; AF009332; AAB64441.1; JOINED.
 DR EMBL; AF009333; AAB64441.1; JOINED.
 DR EMBL; AF009334; AAB64441.1; JOINED.
 DR PIR; A34929; A34929.
 DR HSSP; P01137; IKLA.
 DR InterPro; IPR002400; GF_cys_knot.
 DR InterPro; IPR003911; TGF_TGFB.
 DR InterPro; IPR001839; TGFb_N.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR01423; TGFbPETA.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_beta_1; 1.
 DR Growth factor; Mitogen; Glycoprotein; Signal.
 KM Growth factor; Mitogen; Glycoprotein; Signal.
 FT PROPEP 22
 FT CHAIN 271
 FT DISULFID 277
 FT DISULFID 285
 FT DISULFID 314
 FT DISULFID 314
 FT DISULFID 318
 FT DISULFID 347
 FT CARBOHYD 73
 FT CARBOHYD 123
 FT CARBOHYD 166
 FT CARBOHYD 234
 FT SITE 236
 SQ SEQUENCE 382 AA: 44200 MW: 1034621C917AAE15 CRC64;

Query Match
 Best Local Similarity 40.2%; Score 868.5; DB 1; Length 382;
 Matches 190; Conservative 55; Mismatches 122; Indels 47; Gaps 11;
 9 LPLLLPLMLLVLTGPGRAAGTSTCKTIDMELVKKRIEATRGQLSKRLASPSQGDV 68
 1 MEVLMMLLVLTGPGRAAGTSTCKTIDMELVKKRIEATRGQLSKRLASPSQGDV 68
 69 PPGPLPEALVALYNSTRDVAAGEVPE---PEPEADYVKEVTRVAVESGNOYDK 123
 60 EKMTPPEALVALYNSTRDVAAGEVPE---PEPEADYVKEVTRVAVESGNOYDK 123
 124 FKQTPHSLVLFNLSLEAREPEALVALYNSTRDVAAGEVPE---PEPEADYVKEVTRVAVESGNOYDK 179

Db	116	----	HEPKKFNASHVREYVGNMSLHHHAELRMKYKKQDKDNKDQMLPEFKYQKNGSTH	170
Qy	180	-RLYSNELLAPSDSPSEWLSFDVTVGVYROWLTTRREALIEGRLSAH---	SSDSKDNLTWYE	235
Db	171	SRLESSEYIIPVDDSEMSFDVTKVTYNEWMKRAEENQFCLOPACKCPFPQAKD---	ID	226
Qy	236	INFNSGRGRLDATTIGHM--NRPFLLMATPLERAOHLSSRRRALDTSNYPYDVPDYA	293	
Db	227	IEEG-PALRGDLSLSSKENTKPYLATTSMPAPERIDTVISSRKR-----	270	
Qy	294	SLADLTNYCESSTEKNCCVQOLYIDFRKDIGMKWIIHEPKGYAHNFCLGCPYTWISLDYQ	353	
Db	271	--GVGQCYCEGNGNPGNCVAPLYINFRKDIGMKWIIHEPKGYEANYCIGNCPYIWSMDYQ	328	
Qy	354	SKVIALYINQINPGASAPCCVQALPEPLTVYVYVGRKPKYEOISNNIIVRSCKCS	407	
Db	329	SKVLSLYNQNPPASISPCVDPVLEPLTVYVYVGRKPKYEOISNNIIVRSCKCS	382	
RESULT 13				
TGF3_CHICK				
ID	TGF3_CHICK	STANDARD;	PRT;	412 AA.
AC	P16047;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Transforming growth factor beta 3 precursor (TGF-beta 3).			
GN	TGFB3			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89096956; PubMed=3211158;			
RA	Jakowlew S.B., Dillard P.J., Kondalsh P., Sporn M.B., Roberts A.B.;			
RT	"Complementary deoxyribonucleic acid cloning of a novel transforming			
RT	growth factor-beta messenger ribonucleic acid from chick embryo			
RT	chondrocytes.";			
RL	Mol. Endocrinol. 2:747-755(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=White Leghorn;			
RX	MEDLINE=95169270; PubMed=7865129;			
RA	Burt D.W., Dey B.R., Paton I.R., Morrice D.R., Law A.S.;			
RT	"The chicken transforming growth factor-beta 3 gene: genomic			
RT	structure, transcriptional analysis, and chromosomal location.";			
RL	DNA Cell Biol. 14:111-123(1995).			
RN	[3]			
RP	SEQUENCE OF 1-117 FROM N.A.			
RC	STRAIN=White Leghorn; TISSUE=Blood;			
RX	MEDLINE=92134496; PubMed=1840616;			
RA	Burt D.W., Dey B.R., Paton I.R.;			
RT	"Comparative analysis of human and chicken transforming growth			
RT	factor-beta 2 and -beta 3 promoters.";			
RL	J. Mol. Endocrinol. 7:175-183(1991).			
RN	[4]			
RP	SEQUENCE OF 1-117 FROM N.A.			
RX	MEDLINE=93024487; PubMed=1406706;			
RA	Jakowlew S.B., Lechleider R., Geisler A.G., Kim S.J.,			
RA	Santa-Coloma T.A., Cubert J., Sporn M.B., Roberts A.B.;			
RT	"Identification and characterization of the chicken transforming			
RT	growth factor-beta 3 promoter.";			
RL	Mol. Endocrinol. 6:1285-1298(1992).			
CC	-1- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.			
CC	-1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
CC	-----			
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Query Match	Best Local Similarity	Matches 195; Conservative	Score 852.5; DB 1; Length 412;	Pred. No. 7,6e-61;	Mismatches 117;	Indels 61;	Gaps 14;
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CC	EMBL; M31154; AAA49089.1; -						
DR	EMBL; X58127; CAA41128.2; -						
DR	EMBL; X60055; CAA41128.2; JOINED.						
DR	EMBL; X60091; CAA41128.2; JOINED.						
DR	EMBL; X60090; CAA41128.2; JOINED.						
DR	EMBL; S46000; AAB23575.1; -						
DR	PIR; A34939; A34939.						
DR	HSSP; P10600; 1TGF.						
DR	InterPro; IPRO03911; TGF_TGFB.						
DR	InterPro; IPRO01839; TGFB.						
DR	InterPro; IPRO01111; TGFB.N.						
DR	Pfam; PF00019; TGF_beta.1.						
DR	Pfam; PF00688; TGFB_beta.ProteinIdc; 1.						
DR	PRINTS; PRO1423; TGFbeta.						
DR	Prodom; PD000357; TGFB; 1.						
DR	SMART; SM00204; TGFB; 1.						
DR	PROSITE; PS00250; TGF_BETA.1; 1.						
KM	Growth factor; Mitogen; Glycoprotein; Signal.						
FT	SIGNAL	1	23	POTENTIAL.			
FT	PROPEP	24	300	TRANSFORMING GROWTH FACTOR BETA 3.			
FT	CHAIN	301	412	BY SIMILARITY.			
FT	DISULFID	307	316	BY SIMILARITY.			
FT	DISULFID	315	378	BY SIMILARITY.			
FT	DISULFID	344	409	BY SIMILARITY.			
FT	DISULFID	348	411	BY SIMILARITY.			
FT	DISULFID	377	377	INTERCHAIN (BY SIMILARITY).			
FT	CARBOHYD	74	74	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	135	135	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	142	142	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	SITE	261	263	CELL ATTACHMENT SITE (POTENTIAL).			
FT	CONFLICT	323	326	ELPT -> DFR (IN REF. 1).			
SO	SEQUENCE	412 AA;	47077 MW;	ICAB883170069D55 CRC64;			
QY	15	LMLVLVLTGPRGPAAGCTCTKTIDMELVKKRIEALRGQILSKRLASPSOGDVPDGPPLP	74				
DB	9	LVLISLSTRAIYSLALSSCTTIDLEHIKKRVATINQILSKRLISPRE--SYGPAHY	66				
QY	75	EAVLALYNSTRDRAVAGESEPEPE-----PDADYAKEVTRYLVAF--SGNQYIDKF	124				
DB	67	YQLATLYNSTRELL--EEMEEKEKESCSOENEESEYAKEIHFMDIQGLPHENNELGICP	124				
QY	125	KGRPHSLMYMFNLSERLEAVPEPVLLSRARELRIRL-----KLKVEGHVELYOKYSND--	177				
DB	125	KGVTSVNF--FNVS---SAEKNSTNLFRAEFRVLRAPNPSKRSERIRILFOLRLRDEHI	180				
QY	178	SWRYLSNRLIAPSDSPMLSPDVTGVSQWMLTRBAIEGFRLSAH-----SSDSKD	229				
DB	181	AKRRLYSGRNVQVRGSPENMLSPDVTGVRWMLLRHSNGLFETISIHCPHTFOPNDDIE	240				
QY	230	N--TLHAVELNGNSG--RROGLATL--HGNNRFFLLMTRPRAQH--LHSSHR	278				
DB	241	NLHEVLEIKRGIDSEDDXGGLGRGRIKKOKODLHNPILLMLPRHLESPYLGGOGRKR	300				
QY	279	ALDTNSPYDVDPYASIALDPTNYCFSTSEKNCVROLYIDFRKDLGKMWIHERGYHANF	338				
DB	301	-----ALDNTYCFNRLENCVCVRPLIIEPLFDLGMKWHEKGYFANF	343				
QY	339	CLGCPPTIMSLDLYQSKVALLYNQHNPGASAAACCVQQAELPLIYYVYGRKKRVQLSN	398				
DB	344	CSGCPTLRADSTHTSTVGLNYLTFNLEASASPCVQDLEPLITLITYGRTKRVQLSN	403				
QY	399	MIYRSCKS 407					
DB	404	MYVSKCKS 412					

```

RESULT 14
ID TGF3_PIG STANDARD; PRT; 409 AA.
AC P15203;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 3 precursor (TGF-beta 3).
GN TGF3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ovary;
RX MEDLINE=89091120; PubMed=3208746;
RA Derynck R., Lindquist B., Lee A., Tamm J., Graycar J.L.,
RA Rhee L., Mason A.J., Miller D.A., Coffey R.J., Moses H.L.,
RA Chen E.Y.;
RT "A new type of transforming growth factor-beta, TGF-beta 3."
RL EMBL J. 7:373-374(1988)
CC -1- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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EMBL: X14150; CAA32363.1; -.
PIR: S01825; S01825.
DR HSSP: P10600; ITGJ.
DR InterPro: IPR002400; GF-cysknot.
DR InterPro: IPR003911; TGF_TGFB.
DR InterPro: IPR001839; TGFB.
DR InterPro: IPR001111; TGFB.N.
DR Pfam: PF00019; TGF-beta, 1.
DR Pfam: PF00688; TGFB-propeptide, 1.
DR PRINTS: PR00438; GFCSKNOT.
DR PRINTS: PR01423; TGFBETA.
DR ProDom: PD000357; TGFB. 1.
DR SMART: SM00204; TGFB. 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1..18 POTENTIAL.
FT PROPEP 19..297
FT CHAIN 298..409 TRANSFORMING GROWTH FACTOR BETA 3.
FT DISULFID 304..313 BY SIMILARITY.
FT DISULFID 312..375 BY SIMILARITY.
FT DISULFID 341..406 BY SIMILARITY.
FT DISULFID 345..408 BY SIMILARITY.
FT DISULFID 374..374 INTERCHAIN (BY SIMILARITY).
FT CARBOHD 72..72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 133..133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 140..140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 259..261 CELL ATTACHMENT SITE (POTENTIAL).
FT SEQUENCE 409 AA; 46814 MW; B4900235B5C955E CRC64;
Query Match 38.6%; Score 834; DB 1; Length 409;
Best Local Similarity 44.6%; Pred. No. 2, 3e-59;
Matches 190; Conservative 58; Mismatches 122; Indels 56; Gaps 14;
15 LMLVLVLPGRRAAGSTKTDIMELVKKRRIRAIKQILSKIRLASPPSGDVPPEGLP 74
16 LVLALLNFAVYLSNMSTCTTLDLFDHKKRKAIRKQILSKIRLASPPSPDPSML-ANIP 64

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QY 75 EAVLALYNSTR---DRVAGESVE--PEPEADYIAKEVTRVLMV---ESGNQYIDKFKG 126
DB 65 TQVLDLYNSTRELLEVEHBERGDDCTQENTSESYAKKIKFYMDIQLEHNDLAVCPKG 124
QY 127 TPHSLYMLFNTSELREAVEDEPYLLSRRELRLR-----KLKVEQHVLELXKYSND-----S 178
DB 125 ITSKIFR-FNVSVER-----NENLFRFAEFVLYLMPNPSKRSRSEDRIELFQLOPDEHIAK 180
QY 179 WRYLSNRLIAPSDSEWLSFDVTGVYRWMLTRREAIEGFRISAH-----SSSDSKDN- 230
DB 181 QRYIDGKMLPTRGAAEWLSEFVDVTGVREWLIRRESNIGLEISIHCPCHTQPNDDILENI 240
QY 231 --TLHVEINFGMS-----GRGDLATIGM--NRFLLMPTPLERAQH--LHSSNRRALD 281
DB 241 QEWMEIKRQVDSDDPGRGDLGRLLKKKKEHSPHLLMLTPRDLNPGDGAORRRK-- 297
QY 282 TNSYPYDVPDYASLADLTNYCFSTKNCVCVRLYIDFRKDLGMKWIHEPKGYANFCLG 341
DB 298 -----ALDTNYCFRNLEENCVRPLIYIDFRDLDGMKWHKRGYIANFCSG 343
QY 342 PCPIYLSLDTQYSKVLALYNNHPCASAPCCVQALPEPLIYVYGRKPKVEQLSNMIV 401
DB 344 PCPIYRSADTTHSSVGLYNTLNPEASASPCVQDLEPLIYVYGRKAKVEQLSNMIV 403
QY 402 RSKCS 407
DB 404 KSKCS 409
-----
RESULT 15
ID TGF3_MOUSE STANDARD; PRT; 410 AA.
AC P17125;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 3 precursor (TGF-beta 3).
GN TGF3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90190650; PubMed=2628730;
RA Miller D.A., Lee A., Matsui Y., Chen E.Y., Moses H.L., Derynck R.;
RT "Complementary DNA cloning of the murine transforming growth
RT factor-beta 3 (TGF beta 3) precursor and the comparative expression
RT of TGF beta 3 and TGF beta 1 messenger RNA in murine embryos and
RT adult tissues."
RL Mol. Endocrinol. 3:1926-1934(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91000714; PubMed=2206556;
RA Denhez F., Latyatis R., Kondalish P., Roberts A.B., Sporn M.B.;
RT "Cloning by polymerase chain reaction of a new mouse TGF-beta,
RT mTGF-beta 3."
RL Growth factors 3:139-146(1990).
CC -1- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
-----
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EMBL: M32745; AAA40422.1; -.

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:59:01 ; Search time 37 Seconds
(Without alignments)
1057.479 Million cell updates/sec

Title: US-10-017-372E-37

Perfect score: 2159

Sequence: 1 MAPSGRLRLPLPLMLLV.....GRKKVEQLSNMIVRSCKCS 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*

2: PIR1:**

3: PIR3:**

4: PIR4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2033.5	94.2	390	2 A27512	transforming growth
2	2002	92.7	391	2 S01413	transforming growth
3	1929.5	89.4	390	2 I46463	transforming growth
4	1916.5	88.8	390	1 WPHU2	transforming growth
5	1914.5	88.7	390	2 A26960	transforming growth
6	1893.5	85.0	390	2 JC4023	transforming growth
7	1835.5	85.0	390	1 WPM52	transforming growth
8	1835.5	85.0	390	2 S10219	transforming growth
9	1572.5	72.8	315	2 A40057	transforming growth
10	1047	48.5	373	2 A41918	transforming growth
11	871.5	40.4	412	2 A34939	transforming growth
12	868.5	40.2	382	2 B61036	transforming growth
13	834	38.6	409	2 S01825	transforming growth
14	827.5	38.3	410	2 A41397	transforming growth
15	826.5	38.3	410	2 A55706	transforming growth
16	824.5	38.2	414	2 A36169	transforming growth
17	824	38.2	414	1 WPM52	transforming growth
18	809	37.5	414	1 WPM52	transforming growth
19	809	37.5	414	2 A31249	transforming growth
20	808.5	37.4	413	1 WPM52	transforming growth
21	808	37.4	412	2 A39489	transforming growth
22	793	36.7	442	2 B31249	transforming growth
23	691.5	32.0	130	2 I48196	transforming growth
24	482	22.3	112	2 A61439	transforming growth
25	275	12.6	425	1 I47072	inhibin beta-A cha
26	272.5	12.5	424	1 WPM52	inhibin beta-A cha
27	270.5	12.5	424	1 S31440	inhibin beta-A cha
28	270	12.5	425	1 S50898	inhibin beta-A cha
29	268.5	12.4	426	1 B24248	inhibin beta-A cha

ALIGNMENTS

RESULT 1

A27512 transforming growth factor beta-1 precursor - pig

N:Alternate names: TGF-beta

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 05-Jun-1988 #sequence.revision 05-Jun-1988 #text.change 16-Jul-1999

C/Accession: A27512; A26356; I46557

R:Deruyck, R.; Rhee, L.

Nucleic Acids Res. 15, 3187, 1987

A:Title: Sequence of the porcine transforming growth factor-beta precursor.

A:Reference number: A27512; MUID:87174844; PMID:3470708

A:Molecule type: mRNA

A:Residues: 1-390 <DER>

R:Chelitz, S.; Weatherbee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Mole, J.E.; Lucas, R

Cell 48, 409-415, 1987

A:Title: The transforming growth factor-beta system, a complex pattern of cross-react

A:Reference number: A90890; MUID:87102890; PMID:2879635

A:Accession: A26356

A:Molecule type: protein

A:Residues: 279-322 <CH>

R:Kondiah, P.; Van Obberghen-Schilling, E.; Ludwig, R.L.; Dhar, R.; Sporn, M.B.; Rob

J. Biol. Chem. 263, 18313-18317, 1988

A:Title: CDNA cloning of porcine transforming growth factor-beta 1 mRNAs. Evidence fo

A:Reference number: I46657; MUID:89054010; PMID:2461367

A:Accession: I46657

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-390 <KON>

A:Cross-references: GB:M23703; NID:g755044; PIDN:AAA64616.1; PID:g755045

C:Genetics:

A:Gene: TGF-beta-1

C:Superfamily: Inhibin

C:Keywords: growth factor

Query Match 94.2%, Score 2033.5; DB 2; Length 390;

Best Local Similarity 95.1%; Pred. No. 6.3e-156;

Matches 387; Conservative 0; Mismatches 3; Indels 17; Gaps 1;

QY	1	MAPSGRLRLPLPLMLLVLTGPRPAAGLSTCKTIDMELVYRKRIEATRGILSKRLA	60
DB	1	MPSGRLRLPLPLMLLVLTGPRPAAGLSTCKTIDMELVYRKRIEATRGILSKRLA	60
QY	61	SPPSGQDVPGLPEPAVALINSTRDRAVAGESEPEPEADYVYKEVRYVLVVEGNOI	120
DB	61	SPPSGQDVPGLPEPAVALINSTRDRAVAGESEPEPEADYVYKEVRYVLVVEGNOI	120
QY	121	YDKFGGTHSLYMLFNTSELREAVPEPVLLSRALRLRLKLKVEQHVELYQKYSNDSMR	180
DB	121	YDKFGGTHSLYMLFNTSELREAVPEPVLLSRALRLRLKLKVEQHVELYQKYSNDSMR	180
QY	181	YLSNRLAPSDSPFWLSPDVTGVRQWILTRREAIEGFRLSAHSNDSKNTLHVEINGEN	240

```

Db      181 YLSNRLAPSDSEPELSPDVGVVROWLTRREAIEGFRLSAHSCSDSKDNLHVEINGFN 240
      241 SGRGDDATATGMRNPFLLMATPLERAQHLHSSRRRLADTNSYVDVDTYSLADTN 300
      241 SGRGDDATATGMRNPFLLMATPLERAQHLHSSRRRLADTNSYVDVDTYSLADTN 300
      301 YCFSTERNKCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPCPYIWSLDTQYSKVLA 360
      284 YCFSTERNKCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPCPYIWSLDTQYSKVLA 343
      361 NOHNGASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 407
      344 NOHNGASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 390

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RESULT 2

```

transforming growth factor beta-1 precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Nov-1999
C:Accession: S01413
R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Nucleic Acids Res. 16, 8730, 1988
A:Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-beta 1).
A:Reference number: S01413; MUID:88335639; PMID:3166520
A:Accession: S01413
A:Molecule type: DNA
A:Residues: 1-391 <JAK>
A:Cross-references: EMBL:X12373; NID:963808; PIDN:CAA3093.1; PID:963809
C:Superfamily: Inhibin
C:Keywords: growth factor

```

```

Query Match      92.7%; Score 2002; DB 2; Length 391;
Best Local Similarity 94.1%; Pred. No. 2.2e-153;
Matches 384; Conservative 0; Mismatches 6; Indels 18; Gaps 2;

Db      1 MAFSGRLPLPLPLMLVLTPGRPAAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
      1 MPPSGRLPLPLPLMLVLTPGRPAAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
      61 SPPSGDVPGLPEALVALYNSTRVAGSEVEPEPEADYAKETRYLVAVESGNOI 120
      61 SPPSGDVPGLPEALVALYNSTRVAGSEVEPEPEADYAKETRYLVAVESGNOI 120
      121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLVQHVLYOKYSNDWMR 180
      121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLVQHVLYOKYSNDWMR 180
      181 YLSNRLAPSDSEPELSPDVGVVROWLTRREAIEGFRLSAHSSSDSKDNLHVEINGFN 240
      181 YLSNRLAPSDSEPELSPDVGVVROWLTRREAIEGFRLSAHSSSDSKDNLHVEINGFN 240
      240 NSGRGDLATIHGMNRFLLMATPLERAQHLHSSRRRLADTNSYPYDVDTYSLADTN 299
      241 NSGRGDLATIHGMNRFLLMATPLERAQHLHSSRRRLADTNSYPYDVDTYSLADTN 299
      300 NYCFSTERNKCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPCPYIWSLDTQYSKVLA 359
      284 NYCFSTERNKCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPCPYIWSLDTQYSKVLA 343
      360 YNOHNGASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 407
      344 YNOHNGASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 391

```

```

RESULT 3
146463
transforming growth factor beta-1 - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 24-Nov-1999
C:Accession: I46463; S45115
R:Woodall, C.J.; McLaren, L.J.; Watt, N.J.

```

```

Gene 150, 371-373, 1994
A:Title: Sequence and chromosomal localisation of the gene encoding ovine latent tran
A:Reference number: I46463; MUID:95121932; PMID:7821809
A:Accession: I46463
A:Status: Preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-390 <MOO>
A:Cross-references: EMBL:X76916; NID:9496648; PIDN:CAA54242.1; PID:9496649
A:Note: Submitted to the EMBL Data Library, December 1993
C:Superfamily: Inhibin

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Query Match      89.4%; Score 1929.5; DB 2; Length 390;
Best Local Similarity 89.7%; Pred. No. 1.5e-147;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

Db      1 MAFSGRLPLPLPLMLVLTPGRPAAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
      1 MPPSGRLPLPLPLMLVLTPGRPAAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
      61 SPPSGDVPGLPEALVALYNSTRVAGSEVEPEPEADYAKETRYLVAVESGNOI 120
      61 SPPSGDVPGLPEALVALYNSTRVAGSEVEPEPEADYAKETRYLVAVESGNOI 120
      121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLVQHVLYOKYSNDWMR 180
      121 YDKMKSSHSIYMFNTSELREAVPEVLLSRADVRLRLKLVQHVLYOKYSNDWMR 180
      181 YLSNRLAPSDSEPELSPDVGVVROWLTRREAIEGFRLSAHSSSDSKDNLHVEINGFN 240
      181 YLSNRLAPSDSEPELSPDVGVVROWLTRREAIEGFRLSAHSSSDSKDNLHVEINGFN 240
      241 SGRGDLATIHGMNRFLLMATPLERAQHLHSSRRRLADTNSYPYDVDTYSLADTN 300
      241 SGRGDLATIHGMNRFLLMATPLERAQHLHSSRRRLADTNSYPYDVDTYSLADTN 300
      301 YCFSTERNKCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPCPYIWSLDTQYSKVLA 360
      284 YCFSTERNKCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPCPYIWSLDTQYSKVLA 343
      361 NOHNGASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 407
      344 NOHNGASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 390

```

RESULT 4

```

transforming growth factor beta-1 precursor [validated] - human
N:Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1986 #sequence_revision 19-Oct-1995 #text_change 08-Dec-2000
C:Accession: A27513; A01395; A22290; I59664; S53444
R:Derynck, R.; Rhee, E.Y.; Van Tilburg, A.
Nucleic Acids Res. 15, 3188-3189, 1987
A:Title: Intron-exon structure of the human transforming growth factor-beta precursor
A:Reference number: A27513; MUID:87174845; PMID:3470709
A:Accession: A27513
A:Molecule type: DNA
A:Residues: 1-390 <DER>
A:Cross-references: GB:X05839; GB:X00112; NID:937097; PIDN:CAA29283.1; PID:g1212989
R:Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Eaton, D.H.; Bell, J.R.; Assolian, R.K.; Rob
Nature 316, 701-705, 1985
A:Title: Human transforming growth factor-beta complementary DNA sequence and express
A:Reference number: A01395; MUID:85296301; PMID:3861940
A:Accession: A01395
A:Molecule type: mRNA
A:Residues: 1-9, 'P', 11-24, 'P', 26-159, 'R', 160-390 <DER>
A:Cross-references: GB:X02812; GB:X05114; NID:937092; PIDN:CAA26580.1; PID:g37093
A:Note: The authors suggest that residues 8-23 could represent the hydrophobic core o
R:Massague, J.; Like, B.
J. Biol. Chem. 260, 2636-2645, 1985
A:Title: Cellular receptors for type beta transforming growth factor. Ligand binding
A:Reference number: A22290; MUID:85131019; PMID:2982829
A:Accession: A22290

```

A: Molecule type: protein
 A: Residues: 279-295, 'XX', 298-301 <MAS>
 A: R: Urushizaki, Y.; Nitsui, Y.; Terui, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.; Urushizaki, Tumor Res. 22, 41-55, 1987
 A: Title: Cloning and expression of the gene for human transforming growth factor-beta 1
 A: Reference number: 159664
 A: Accession: 159664
 A: Molecule type: mRNA
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Residues: 279-390 <RSS>
 A: Cross-references: GB:M38449; NID:9339557; PIDN:AAA36735.1; PID:9339558
 A: R: Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyoe, D.; Chait, B.T.; Marshak, D.R. Biochem. J. 305, 87-92, 1995
 A: Title: Physical and biological characterization of a growth-inhibitory activity purified from human placenta
 A: Reference number: S53444; MUID:95126934; PMID:7826358
 A: Accession: S53444
 A: Status: preliminary
 A: Molecule type: protein
 A: Residues: 279-297 <STA>
 C: Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide C: Genetics:
 A: Gene: GDB: TGFBI; TGFBI
 A: Cross-references: GDB: 120729; OMIM: 190180
 A: Map position: 19q13.2-19q13.2
 C: Superfamily: Inhibin
 C: Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation
 F: 1-18/Domain: signal sequence #status predicted <SIG>
 F: 19-278/Domain: propeptide #status predicted <PRO>
 F: 244-246/Region: cell attachment (R-G-D) motif
 F: 279-390/Product: transforming growth factor beta-1 #status experimental <MAT>
 F: 82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.8%; Score 1916.5; DB 1; Length 390;
 Best Local Similarity 89.7%; Pred. No. 1.7e-146;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRRIEATRGQILSKRLA 60
 DB 1 MPSPGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRRIEATRGQILSKRLA 60
 QY 61 SPSPGVDVPGPLPEAVLALYNSTRDRAVAGESEVEPEPEADYAKETRVLMVESGNOI 120
 DB 61 SPSPGVDVPGPLPEAVLALYNSTRDRAVAGESEVEPEPEADYAKETRVLMVESGNOI 120
 QY 121 YDKERKTPSHLYMFLNTSELREAVPEPVLLSRALRLRLKLEQVHVELYOKYSNDSMR 180
 DB 121 YDKERKTPSHLYMFLNTSELREAVPEPVLLSRALRLRLKLEQVHVELYOKYSNDSMR 180
 QY 181 YLSNRLAPSDPEMISFDYGVGVQWLTREALEIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 DB 181 YLSNRLAPSDPEMISFDYGVGVQWLTREALEIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 241 SGRGDLATIHGMNRPFLMATPLERAQHLHSSRRRALDNTSYRYDVYASLADTN 300
 DB 241 SGRGDLATIHGMNRPFLMATPLERAQHLHSSRRRALDNTSYRYDVYASLADTN 300
 QY 301 YCFSTTEKNCVROLYIDFRKDLGKWIHEPKGYHANFCIPCIYMSLDTOYSKVLYALY 360
 DB 301 YCFSTTEKNCVROLYIDFRKDLGKWIHEPKGYHANFCIPCIYMSLDTOYSKVLYALY 360
 QY 361 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 407
 DB 361 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 407
 QY 344 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 390
 DB 344 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 5
 A26960
 transforming growth factor beta-1 precursor - green monkey
 C: Species: Cercopithecus aethiops (green monkey, grivet)
 C: Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 24-Nov-1999
 C: Accession: A26960
 R: Sharples, K.; Ploewman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F.
 DNA 6, 239-244, 1987

A: Title: Cloning and sequence analysis of simian transforming growth factor-beta cDNA
 A: Reference number: A26960; MUID:87246074; PMID:3474130
 A: Accession: A26960
 A: Molecule type: mRNA
 A: Residues: 1-390 <SHA>
 A: Cross-references: GB:M16658; NID:9176552; PIDN:AAA35369.1; PID:9176553
 C: Superfamily: Inhibin
 C: Keywords: growth factor
 F: 1-16/Domain: signal sequence #status predicted <SIG>
 F: 17-390/Product: transforming growth factor beta #status predicted <MAT>
 F: 17-390/Product: transforming growth factor beta #status predicted <MAT>

Query Match 88.7%; Score 1914.5; DB 2; Length 390;
 Best Local Similarity 89.4%; Pred. No. 2.4e-146;
 Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRRIEATRGQILSKRLA 60
 DB 1 MPSPGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRRIEATRGQILSKRLA 60
 QY 61 SPSPGVDVPGPLPEAVLALYNSTRDRAVAGESEVEPEPEADYAKETRVLMVESGNOI 120
 DB 61 SPSPGVDVPGPLPEAVLALYNSTRDRAVAGESEVEPEPEADYAKETRVLMVESGNOI 120
 QY 121 YDKERKTPSHLYMFLNTSELREAVPEPVLLSRALRLRLKLEQVHVELYOKYSNDSMR 180
 DB 121 YDKERKTPSHLYMFLNTSELREAVPEPVLLSRALRLRLKLEQVHVELYOKYSNDSMR 180
 QY 181 YLSNRLAPSDPEMISFDYGVGVQWLTREALEIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 DB 181 YLSNRLAPSDPEMISFDYGVGVQWLTREALEIEGFRLSAHSSSDSKDNTLHVEINGFN 240
 QY 241 SGRGDLATIHGMNRPFLMATPLERAQHLHSSRRRALDNTSYRYDVYASLADTN 300
 DB 241 SGRGDLATIHGMNRPFLMATPLERAQHLHSSRRRALDNTSYRYDVYASLADTN 300
 QY 301 YCFSTTEKNCVROLYIDFRKDLGKWIHEPKGYHANFCIPCIYMSLDTOYSKVLYALY 360
 DB 301 YCFSTTEKNCVROLYIDFRKDLGKWIHEPKGYHANFCIPCIYMSLDTOYSKVLYALY 360
 QY 361 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 407
 DB 361 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 407
 QY 344 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 390
 DB 344 NOHNPASAPCCVPOALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 6
 JC4023
 transforming growth factor beta-1 - dog
 C: Species: Canis lupus familiaris (dog)
 C: Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 24-Nov-1999
 C: Accession: JC4023
 R: Manning, A.M.; Auchampach, J.A.; Drong, R.F.; Slightom, J.L.
 Gene 155, 307-308, 1995
 A: Title: Cloning of a canine cDNA homologous to the human transforming growth factor-
 A: Reference number: JC4023; MUID:95237630; PMID:7721110
 A: Accession: JC4023
 A: Molecule type: mRNA
 A: Residues: 1-390 <MAN>
 A: Cross-references: GB:I34956; NID:9516071; PIDN:AAA51458.1; PID:9516072
 C: Comment: This factor plays a multifunctional role as a regulator of mammalian cell
 C: Genetics:
 A: Gene: tgfb-beta1
 C: Superfamily: Inhibin
 C: Keywords: growth factor; transforming protein
 F: 288-390/Product: transforming growth factor beta 1 #status predicted <MAT>

Query Match 87.7%; Score 1893.5; DB 2; Length 390;
 Best Local Similarity 88.7%; Pred. No. 1.2e-144;
 Matches 361; Conservative 12; Mismatches 17; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRRIEATRGQILSKRLA 60
 DB 1 MPSPGRLPLPLPLMLVLTGPRPAGLSTCKTIDMELVKKRRIEATRGQILSKRLA 60

DB 284 YCFSSSTKNCVROLIDFRKDLGKMKIHPEKGYHANFCLGPCPYIWSLDTQYSKVLA 343

QY 361 NQHNRPASAPCCVPQALPEPLIYVYVGRKPKVEQLSNMIVRSCKCS 407

DB 344 NQHNRPASAPCCVPQALPEPLIYVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 9

A40057

transforming growth factor beta-1 precursor - bovine (fragment)

N:Alternate names: beta-TGF; cartilage-inducing factor-A; EGF-dependent TGF or deGF; MGF

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Feb-1992 #sequence-revision 28-Feb-1992 #text-change 16-Jul-1999

C:Accession: A40057; A42320; A05284; A24322; B61439

R:Man Obberghen-Schilling, E.; Kondratiah, P.; Ludwig, R.L.; Sporn, M.B.; Baker, C.C.

Mol. Endocrinol. 1, 693-698, 1987

A:Title: Complementary deoxyribonucleic acid cloning of bovine transforming growth factor

A:Reference number: A40057; MUID:91042552; PMID:3153459

A:Accession: A40057

A:Molecule type: mRNA

A:Residues: 1-315 <VAN>

A:Cross-references: GB:M36271; NID:g163747; PIDN:AAA30778.1; PID:g163748

R:Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.J.; Glaser, C.B.

J. Biol. Chem. 267, 2325-2328, 1992

A:Title: Purification and characterization of transforming growth factor-beta2.3 and -beta

A:Reference number: A42320; MUID:92129307; PMID:1733936

A:Accession: A42320

A:Molecule type: Protein

A:Residues: 204-209, 'X', 211-217 <OGA>

R:Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan, Y.C.E.; Stein

Biochemistry 22, 5692-5698, 1993

A:Title: Purification and properties of a type beta transforming growth factor from bovi

A:Reference number: A05284; MUID:84104793; PMID:6607069

A:Accession: A05284

A:Molecule type: Protein

A:Residues: 204-218 <ROB>

R:Sejedin, S.M.; Thompson, A.Y.; Bentz, H.; Rosen, D.M.; McPherson, J.M.; Conti, A.; Sig

J. Biol. Chem. 261, 5693-5695, 1986

A:Title: Cartilage-inducing factor-A. Apparent identity to transforming growth factor-be

A:Reference number: A24322; MUID:86195954; PMID:3754555

A:Accession: A24322

A:Molecule type: Protein

A:Residues: 204-233 <SEY>

R:Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.

J. Protein Chem. 10, 565-575, 1991

A:Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta

A:Reference number: A61439; MUID:92189724; PMID:1799413

A:Accession: B61439

A:Molecule type: protein

A:Residues: 204-209, 'X', 211-217, 'XX', 220-232 <JIN>

C:Comment: This polypeptide is composed of two polypeptide chains cross-linked by disulf

C:Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic mitogenic a

tion. Cells grown in monolayer do not respond in a similar manner to these growth factors

C:Superfamily: Inhibin

C:Keywords: glycoprotein; growth factor; heterodimer

F:204-315/Product: transforming growth factor beta-1 #status experimental <MAT>

F:7,61,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.8%; Score 1572.5; DB 2; Length 315;

Best Local Similarity 88.9%; Pred. No. 6, 1e-119;

Matches 295; Conservative 9; Mismatches 11; Indels 17; Gaps 1;

DB 76 AYALATNSTRDRVAGSEVPEPEADYAKETRYVLAVESGNOYDKFKGTPHSLYLF 135

QY 136 NITSELREAVEPEVLLSRALRLRLKLVKQVHLYOKYSNDSRRYISNRLLASDSPEW 195

DB 61 NITSELREAVEPEVLLSRADYRLRLKLVKQVHLYOKYSNDSRRYISNRLLASDSPEW 120

QY 196 LSPDYGVAVQWILTRRAITGFRLSAHSSSDSKDNTLHVEINSGRRGDLATIHGMNR 255

DB 121 LSPDYGVAVQWILTRREIEIGFRLSAHSCSDSKDNTLQVDINGESSGRKGLATIHGMNR 180

QY 256 PELLMAFPLERAQHSHSRHRRALDTNSYPYDVPYASLALDTNCFSTKNCVROL 315

DB 181 PELLMAFPLERAQHSHSRHRR-----ADLTNCFSTKNCVROL 223

QY 316 YIDFRKDLGKMKIHPEKGYHANFCLGPCPYIWSLDTQYSKVLA 375

DB 224 YIDFRKDLGKMKIHPEKGYHANFCLGPCPYIWSLDTQYSKVLA 283

QY 376 QALEPLIYVYVGRKPKVEQLSNMIVRSCKCS 407

DB 284 QALEPLIYVYVGRKPKVEQLSNMIVRSCKCS 315

RESULT 10

A41918

transforming growth factor beta-4 precursor - chicken (fragment)

N:Alternate names: TGF-beta 4

C:Species: Gallus gallus (chicken)

C:Date: 31-Dec-1993 #sequence-revision 31-Dec-1993 #text-change 16-Jul-1999

C:Accession: A41918; A34941; S03110

R:Butt, D.W.; Jakowlew, S.B.

Mol. Endocrinol. 6, 989-992, 1992

A:Title: Correction: a new interpretation of a chicken transforming growth factor-bet

A:Reference number: A41918; MUID:92357039; PMID:1353860

A:Accession: A41918

A:Molecule type: mRNA

A:Residues: 1-373 <BUR>

A:Cross-references: GB:M31160; GB:X08012; GB:SA1706; NID:g1262437; PIDN:AB05637.1; P

A:Note: sequence extracted from NCBI backbone (NCBI:110186, NCBI:110187)

R:Jakowlew, S.B.; Dillard, P.D.; Sporn, M.B.; Roberts, A.B.

Mol. Endocrinol. 2, 1186-1195, 1988

A:Title: Complementary deoxyribonucleic acid cloning of a messenger ribonucleic acid

A:Reference number: A34941; MUID:89112198; PMID:2464131

A:Accession: A34941

A:Molecule type: mRNA

A:Residues: 1-MDPMISGCGSGSPRPPTAPWSIGSRRTASSCGTSRKYRAVEGRL, 122-209, 'D', 211-37

A:Cross-references: EMBL:X08012

C:Superfamily: Inhibin

C:Keywords: glycoprotein; growth factor

F:1/Domain: signal sequence (fragment) #status predicted <SIG>

F:223-225/Region: cell attachment (R-G-D) motif

F:260-373/Product: transforming growth factor beta-4 #status predicted <MAT>

F:54,109,153/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 48.5%; Score 1047; DB 2; Length 373;

Best Local Similarity 52.9%; Pred. No. 1, 6e-76;

Matches 207; Conservative 52; Mismatches 100; Indels 32; Gaps 8;

DB 30 LSTCKTIMELVKKRRIRKRIEAINQILSKLRLASPPSOGDVPQGLPRAVLALYNSTRDRA 89

QY 2 LSTCKTLDLEAKKKRIEAVRQILSKLRLTAPPASETPPRLPDVRLALNSTQELK 61

DB 90 GFS-VEPEPEADYAKETRYVLAVESGNOYDKFKGTPHSLYLFNITSELREAVEPEV 148

QY 62 QRARLRPPDGDDEYAKELRIPMETTWGDAEMHQPOSHSTFFPNVSRARRG-GRPT 120

DB 149 LLSRAELRLRLKLVKQVHLYOKYSNDSRRYISNRLLASDSPEWLSFDVTGV 203

QY 121 LLSRAELRLRLKLVKQVHLYOKYSNDSRRYISNRLLASDSPEWLSFDVTGV 180

DB 204 VROWLTTRRAITGFRLSAHSSSD--SKDNTLHVEINSGRRGDLATIHGMNR--PFL 258

QY 181 VROWLTTRRAITGFRLSAHSSSD--SKDNTLHVEINSGRRGDLATIHGMNR--PFL 239

DB 259 LTMAPPLERAQHSHSRHRRALDTNSYPYDVPYASLALDTNCF--SSTKNCVROL 316

QY 240 LTMAPPLERAQHSHSRHRRALDTNSYPYDVPYASLALDTNCF--SSTKNCVROL 282

DB 317 IDFRKDLGKMKIHPEKGYHANFCLGPCPYIWSLDTQYSKVLA 376

Db 227 IEGF-PALRGDLASLSKENTKPYLMTSMAPERIDVTSSKKR----- 270

Oy 294 SLALDNTNCCSSTKNCVROLYIDERRDLGKWIHEBKGYHANFCLGPCYIYSLDTQY 353

Db 271 --GVGEYECGNGNPGNCVPLIYINFRKDLGKWIHEBKGYEANYCIGNCPYISMDOY 328

Oy 354 SKYLAITYNHNPGASAPCCVPALEPLIYIYVGRKPKVQOLSMTIYRSCKS 407

Db 329 SKYLSIYNHNPGASISPCCVPALEPLIYIYVGRKPKVQOLSMTIYRSCKS 382

RESULT 13

Transforming growth factor beta-3 precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999

C:Accession: S01825

R:Derynck, R.; Landquist, P.B.; Lee, A.; Wen, D.; Tamm, J.; Graycar, J.L.; Rhee, L.; Mas EMBO J 7, 3737-3743, 1988

A:Title: A new type of transforming growth factor-beta, TGF-beta3.

A:Reference number: S01824; MUID:89031120; PMID:3208746

A:Accession: S01825

A:Molecule type: mRNA

A:Residues: 1-409 <DER>

A:Cross-references: EMBL:X14150; NID:92127; PIDN:CAA32363.1; PID:92128

C:Superfamily: Inhibin

C:Keywords: growth factor

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-297/Domain: propeptide #status predicted <PRO>

F:298-409/Product: transforming growth factor beta-3 #status predicted <MAT>

Query Match 38.6%; Score 834; DB 2; Length 409;

Best Local Similarity 44.6%; Pred. No. 2.6e-59;

Matches 190; Conservative 58; Mismatches 122; Indels 56; Gaps 14;

Oy 15 LLMVLVTPGRPAAGLSTCKTIDMELVKRRKIEAIRGOILSKRLASPPSGDVPPEPLP 74

Db 7 LVLALLNFATVLSISMSTCTLDPDHKKRVEAIRGOILSKRLTSPDPSML--ANIP 64

Oy 75 EAVLALYNSTR---DRVAGESEV--PEPEPADYAKETRYLVM---ESGNOIYDKFKG 126

Db 65 YQVLDLYNSTRELLEEVHGERDCTQENTSEYAKETRYKEDMTQGLEHNDLAVCPKG 124

Oy 127 TPHSLYMFTNSELREAVPEVLLSRARLRLRL---KLKVEOHVELYQKYSND---S 178

Db 125 ITSKEFR-FNVSSVSK---NETNLFRAEFRVLRMPSPSSKRSQRLEIQLDPDEHIAK 180

Oy 179 WRYSLNRLAPSDSPFWLSFDVTGYVROWLTPREALTEGFRLSAH-----SSDSKDN- 230

Db 181 QRYIDGKNLPFRGAEMLSFDVTGYVROWLTPREALTEGFRLSAH-----SSDSKDN- 240

Oy 231 --TLHVEINGNS---GRGDLATIGHM--NRPELLMATPLERAOH--LHSSRRRALD 281

Db 241 QEVMEIRKRGVSEDDPGGDLGRLLKKKSHSHLLTMMIPRDLNPGLAGAORKKR--- 297

Oy 282 TNSYPRVDPAVSLADLTNYCFSSTEKNCVROLYIDFRKDLGKWIHEBKGYHANFCLG 341

Db 288 -----ALDTNYCFRNLEENCCVRLIYIDFRQDLGKWKWIHEBKGYANFCSG 343

Oy 342 PCPYIWSLDTQYSKYLAITYNHNPGASAPCCVPALEPLIYIYVGRKPKVQOLSMTIY 401

Db 344 PCPYIRASADTTHSSVLYGLYNTLNPEASASPCVPALEPLIYIYVGRKPKVQOLSMTIY 403

Oy 402 :||||| 407

Db 404 KSKCS 409

RESULT 14

A41397

Transforming growth factor beta-3 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 16-Jul-1999

C:Accession: A41397; A61039; A61225

R:Miller, D.A.; Lee, A.; Matsui, Y.; Chen, E.Y.; Moses, H.L.; Derynck, R. Mol. Endocrinol. 3, 1926-1934, 1989

A:Title: Complementary DNA cloning of the murine transforming growth factor-beta3 (TGF-beta3).

A:Reference number: A41397; MUID:90190650; PMID:2628730

A:Accession: A41397

A:Molecule type: mRNA

A:Residues: 1-410 <MUI>

A:Cross-references: GB:M32745; NID:9201949; PIDN:AAA0422.1; PID:9201950

R:Denhez, F.; Lafyatis, R.; Kondratiah, P.; Roberts, A.B.; Sporn, M.B.

A:Title: Cloning by polymerase chain reaction of a new mouse TGF-beta3.

A:Reference number: A61039; MUID:91000714; PMID:2206556

A:Accession: A61039

A:Molecule type: mRNA

A:Residues: 1-410 <DEN>

R:Watlin, F.; Scotto, L.; Assoian, R.K.; Wolgemuth, D.J.

Cell Growth Differ. 2, 77-83, 1991

A:Title: Cell lineage specificity of expression of the murine transforming growth fac

A:Reference number: A61225; MUID:91295576; PMID:2069871

A:Accession: A61225

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 285-410 <MAT>

C:Superfamily: Inhibin

C:Keywords: glycoprotein; growth factor; growth regulation

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-268/Domain: propeptide #status predicted <PRO>

F:269-410/Product: transforming growth factor beta-3 #status predicted <MAT>

F:72,133,140/Binding site: carbohydate (Asn) (covalent) #status predicted

Query Match 38.3%; Score 827.5; DB 2; Length 410;

Best Local Similarity 44.2%; Pred. No. 8.6e-59;

Matches 188; Conservative 57; Mismatches 127; Indels 53; Gaps 13;

Oy 15 LLMVLVTPGRPAAGLSTCKTIDMELVKRRKIEAIRGOILSKRLASPPSGDVPPEPLP 74

Db 7 LVLALLNFATVLSISMSTCTLDPDHKKRVEAIRGOILSKRLTSPDPSML--HNP 64

Oy 75 EAVLALYNSTR---DRVAGESEV--PEPEPADYAKETRYLVM---ESGNOIYDKFKG 126

Db 65 YQVLDLYNSTRELLEEVHGERDCTQENTSEYAKETRYKEDMTQGLEHNDLAVCPKG 124

Oy 127 TPHSLYMFTNSELREAVPEVLLSRARLRLRL---KLKVEOHVELYQKYSND---S 178

Db 125 ITSKEFR-FNVSSVSK---NETNLFRAEFRVLRMPSPSSKRSQRLEIQLDPDEHIAK 180

Oy 179 WRYSLNRLAPSDSPFWLSFDVTGYVROWLTPREALTEGFRLSAH-----SSDSKDN- 230

Db 181 QRYIDGKNLPFRGAEMLSFDVTGYVROWLTPREALTEGFRLSAH-----SSDSKDN- 240

Oy 231 --TLHVEINGNS---GRGDLATIGHM--NRPELLMATPLERAOH--LHSSRRRALD 282

Db 241 HEVMEIRKGVNEDDHGGDLGRLLKKKQKHNNPHILMIPRHLNDSQGSQKR----- 296

Oy 283 TNSYPRVDPAVSLADLTNYCFSSTEKNCVROLYIDFRKDLGKWIHEBKGYHANFCLG 342

Db 287 -----KRALDTNYCFRNLEENCCVRLIYIDFRQDLGKWKWIHEBKGYANFCSG 345

Oy 343 CPYIWSLDTQYSKYLAITYNHNPGASAPCCVPALEPLIYIYVGRKPKVQOLSMTIY 402

Db 346 CPYIRASADTTHSSVLYGLYNTLNPEASASPCVPALEPLIYIYVGRKPKVQOLSMTIY 405

Oy 403 SCKCS 407

Db 406 SCKCS 410

RESULT 15

A55706

Transforming growth factor beta-3 precursor - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 16-Jul-1999
Accession: A55706. RALN00. 51607
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 16-Jul-1999

B. Wand T. : Kuliszowski M. : yoo

J. Biol. Chem. 270: 2722-2728, 1995

A: Title: Cloning and expression of a novel

A; Reference number: A55706; MUID:95155340; PMID:7852342

Accession: A55706

A; molecule type: mk

A;Residues: 1-410 <WAW>

A;Cross-references: GB:U03491

A;Note: it is uncertain whether

R:McKinnon, R.D.: Piras, G.: Ida, T.A.: Dubois-Da

Cell Biol 121 1397-1407 1993
Dobbs-Dalcq, M

3-12-13, 135, 140, 155

10. Reference number: 140500. Title: α -Bref-A in oligodendrocyte differentiation.

A; reference number: A40699; MUID:93286190; PMID:8509457

A; Accession: B40695

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 157-211 <MCK>

A;Cross-references: EMBL:X71903. NTD:α311326. PTDN:CA50722 1. PTD:α311327

C:Superfamily: inhibin

Query Match	Score	DB 2	Length
38.38	826.5	410	

Best Local Similarity 44.28; Pred. No. 1e-58;

Matches 188; Conservative 57; Mismatches 127; Indels 53; Gaps 13.

15 LVLVLTTPGPAAGLSTCKTIDMELVKRRRIEATRGOTT,SKI,PTASPPSOGNVPBPBP 74

[illegible]

7	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
7	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

75 FAVORABLE VIEWS

1 2 EAVLALINSIK--PEPEEADYYAKEVTRVLMVE--SGNQIYDKFKG 12

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65 YQVLALYNSTRELL EEMHGEREGCTQETSESEYYAKEIHKFDMIOGLAEHNEI LVC PKG 12

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127 TPHSLYMLENTSELREAVPEPVILSRAEIRI.I.BI.-----KI.KVEOHVET.YOKVSN-----S 17

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125 ITSKYEB-FNVSSVEK---NGTNI PPAFFBYT DVBNDCCKPMEORIRI HOI DDDDDDDDD 10

NOINDEKKEFVLEVPFSSKRIEQRLELEQLLRPDEHTAK 18

179 WPYTSNBT ABCEDEFW CENUEU/CI/NOU EEEFZ EEEEEE...

1 / 2 MNIUSNUEAFSDSEWLSFVJIGV KQW LIRKREAL EGF KLSAH-----SSSDSKDN- 23

[illegible]

181 QRYIGKNLPTRGTAEWLSFDVTDTVREWLLRKRESNLGLEISIHCPCHTFQPNGDILENV 24

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Searched: 262574 seqs, 29422922 residues

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	1919.5	88.9	390	1	US-08-132-405-1
2	1919.5	88.9	390	1	US-08-395-939A-1
3	1919.5	88.9	390	5	PCT-US91-01861-1
4	1919.5	88.9	390	6	5168051-2
5	1914.5	88.7	390	1	US-07-669-171-2
6	1909	88.4	394	5	PCT-US94-03705-5
7	828.5	38.4	412	1	US-08-132-405-3
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9	824.5	38.2	412	4	US-09-380-662-21
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11	824.5	38.2	412	6	5262319-2
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13	809	37.5	414	1	US-08-132-405-2
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15	809	37.5	414	5	PCT-US94-03705-6
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21	800.5	37.1	455	6	5221620-2
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24	638	29.6	112	1	US-07-979-841-1
25	638	29.6	112	1	US-08-197-792-36
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28	638	29.6	112	1	US-08-459-214-36	Sequence 36, Appl
29	638	29.6	112	1	US-08-470-837-30	Sequence 40, Appl
30	638	29.6	112	2	US-08-789-588-41	Sequence 31, Appl
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32	638	29.6	112	3	US-09-123-233-2	Sequence 2, Appl
33	638	29.6	112	3	US-08-927-433-5	Sequence 5, Appl
34	638	29.6	112	3	US-08-868-452-30	Sequence 30, Appl
35	638	29.6	112	5	PCT-US93-03068-1	Sequence 1, Appl
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39	638	29.6	114	3	US-08-946-092A-21	Sequence 21, Appl
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ALIGNMENTS

RESULT 1
US-08-132-405-1
; Sequence 1, Application US/08132405

; Patent No. 5409896

; GENERAL INFORMATION:

; APPLICANT: Ammann, Arthur J.

; APPLICANT: Rudman, Christopher G.

; TITLE OF INVENTION: Method of Inducing Bone Growth Using

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/132,405

; FILING DATE: 06-OCT-1993

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/063841

; FILING DATE: 18-MAY-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/790856

; FILING DATE: 12-NOV-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/401906

; FILING DATE: 01-SEP-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Hasak, Janet E.

; REGISTRATION NUMBER: 28,616

; REFERENCE/DOCKET NUMBER: 597D1C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1896

; TELEFAX: 415/952-9881

; TELETYPE: 910/371-7168

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 390 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; US-08-132-405-1

Query Match 88.9%; Score 1919.5; DB 1; Length 390;
 Best Local Similarity 89.7%; Pred. No. 3e-169;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCTIDMELVKKRIEAIKQILSKRLA 60
 1 MPPSGRLPLPLPLMLVLTGPRPAGLSTCTIDMELVKKRIEAIKQILSKRLA 60
 61 SPPSGDVPPEPLPEAVLALYNSTRDVAGSEVPEPEPEADYAKETRYLVWESGNOI 120
 61 SPPSGDVPPEPLPEAVLALYNSTRDVAGSEVPEPEPEADYAKETRYLVWESGNOI 120
 61 SPPSGDVPPEPLPEAVLALYNSTRDVAGSEVPEPEPEADYAKETRYLVWESGNOI 120
 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLYEQHVELYKXYSNDSWR 180
 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLYEQHVELYKXYSNDSWR 180
 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLYEQHVELYKXYSNDSWR 180
 181 YLSNRLAASDSPEWLSFDYGVVROWLSRGELEGFRLSAHSCSDSDNTLQVDINGFT 240
 181 YLSNRLAASDSPEWLSFDYGVVROWLSRGELEGFRLSAHSCSDSDNTLQVDINGFT 240
 241 SGRGDLATIGHMNRPFLLMATPLERAQHLSSRRRLADTNSYPDYVASYALADTN 300
 241 SGRGDLATIGHMNRPFLLMATPLERAQHLSSRRRLADTNSYPDYVASYALADTN 300
 301 YCFSSTEKNCVQOLYIDFRKDLGKWIHEPKGYHANFCLGPCPYTMSLDTQYSKVALY 360
 284 YCFSSTEKNCVQOLYIDFRKDLGKWIHEPKGYHANFCLGPCPYTMSLDTQYSKVALY 343
 361 NQHNPGASAPCCVQALPEPLPIYVYGKPKVQVOLSNNMIVRSCKS 407
 344 NQHNPGASAPCCVQALPEPLPIYVYGKPKVQVOLSNNMIVRSCKS 390

RESULT 2
 US-08-395-939A-1
 Sequence 1, Application US/08395939A
 Patent No. 5604204
 GENERAL INFORMATION:
 APPLICANT: Ammann, Arthur J.
 APPLICANT: Rudman, Christopher G.
 TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE
 TITLE OF INVENTION: GROWTH
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/395, 939A
 FILING DATE: 27-FEB-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/132405
 FILING DATE: 12-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/063841
 FILING DATE: 18-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/790856
 FILING DATE: 12-NOV-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/401906
 FILING DATE: 1-SEP-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.

REGISTRATION NUMBER: 28,616
 REFERENCE/DOCKET NUMBER: P0597D1C2D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1896
 TELEFAX: 415/952-9881
 TELEFAX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-395-939A-1

Query Match 88.9%; Score 1919.5; DB 1; Length 390;
 Best Local Similarity 89.7%; Pred. No. 3e-169;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTGPRPAGLSTCTIDMELVKKRIEAIKQILSKRLA 60
 1 MPPSGRLPLPLPLMLVLTGPRPAGLSTCTIDMELVKKRIEAIKQILSKRLA 60
 61 SPPSGDVPPEPLPEAVLALYNSTRDVAGSEVPEPEPEADYAKETRYLVWESGNOI 120
 61 SPPSGDVPPEPLPEAVLALYNSTRDVAGSEVPEPEPEADYAKETRYLVWESGNOI 120
 61 SPPSGDVPPEPLPEAVLALYNSTRDVAGSEVPEPEPEADYAKETRYLVWESGNOI 120
 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLYEQHVELYKXYSNDSWR 180
 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLYEQHVELYKXYSNDSWR 180
 121 YDKFKGTPHSLYMLFNTSELREAVPEVLLSRAELRLRLKLYEQHVELYKXYSNDSWR 180
 181 YLSNRLAASDSPEWLSFDYGVVROWLSRGELEGFRLSAHSCSDSDNTLQVDINGFT 240
 181 YLSNRLAASDSPEWLSFDYGVVROWLSRGELEGFRLSAHSCSDSDNTLQVDINGFT 240
 241 SGRGDLATIGHMNRPFLLMATPLERAQHLSSRRRLADTNSYPDYVASYALADTN 300
 241 SGRGDLATIGHMNRPFLLMATPLERAQHLSSRRRLADTNSYPDYVASYALADTN 300
 301 YCFSSTEKNCVQOLYIDFRKDLGKWIHEPKGYHANFCLGPCPYTMSLDTQYSKVALY 360
 284 YCFSSTEKNCVQOLYIDFRKDLGKWIHEPKGYHANFCLGPCPYTMSLDTQYSKVALY 343
 361 NQHNPGASAPCCVQALPEPLPIYVYGKPKVQVOLSNNMIVRSCKS 407
 344 NQHNPGASAPCCVQALPEPLPIYVYGKPKVQVOLSNNMIVRSCKS 390

RESULT 3
 PCT-US91-01861-1
 Sequence 1, Application PC/TUS9101861
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 TITLE OF INVENTION: Method of Pre-disposing Mammals to
 TITLE OF INVENTION: Accelerated Tissue Repair
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/01861
 FILING DATE: 19910320
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. Ser. No. 07/504,495
 FILING DATE: 4 April 1990

ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E. 28, 616
 REGISTRATION NUMBER: 28, 616
 REFERENCE/DOCKET NUMBER: 637
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/266-1896
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 PCT-US91-01661-1

Query Match 88.9%; Score 1919.5; DB 5; Length 390;
 Best Local Similarity 89.7%; Pred. No. 3e-169;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 DB 1 MPSPGLRLPLPLMLVLTTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 QY 61 SPSPGDVPPGPPEAVLALYNSTRDVAGSEVPEPEPEADYYAKETRVLMVESGNOI 120
 DB 61 SPSPGDVPPGPPEAVLALYNSTRDVAGSEVPEPEPEADYYAKETRVLMVETHEI 120
 QY 121 YDKFKGTPHSLYMLFNTSELRVAVPEVLLSRALRLRLKLYEQHVELYQKYSNDSMR 180
 DB 121 YDKFKGTPHSLYMLFNTSELRVAVPEVLLSRALRLRLKLYEQHVELYQKYSNDSMR 180
 QY 121 YDKFKGTPHSLYMLFNTSELRVAVPEVLLSRALRLRLKLYEQHVELYQKYSNDSMR 180
 DB 121 YDKFKGTPHSLYMLFNTSELRVAVPEVLLSRALRLRLKLYEQHVELYQKYSNDSMR 180
 QY 181 YLSNRLAPSDSPWLSFDYTGVRQWLSRGEIEGFRLSAHSCSDSDNTLOVDINGFT 240
 DB 181 YLSNRLAPSDSPWLSFDYTGVRQWLSRGEIEGFRLSAHSCSDSDNTLOVDINGFT 240
 QY 241 SGRGDLATIHGMNRPFLMLATPLERAQHLSSRRRALDTSYDYVASYALDTN 300
 DB 241 TGRGDLATIHGMNRPFLMLATPLERAQHLSSRRRALDTSYDYVASYALDTN 283
 QY 301 YCFSTTEKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVLALY 360
 DB 301 YCFSTTEKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVLALY 360
 QY 284 YCFSTTEKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVLALY 343
 DB 284 YCFSTTEKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVLALY 343
 QY 361 NOHNPASAPCCVPQALEPLIYVYVGRKPKVEOLSNMIVRSCKS 407
 DB 361 NOHNPASAPCCVPQALEPLIYVYVGRKPKVEOLSNMIVRSCKS 390
 QY 344 NOHNPASAPCCVPQALEPLIYVYVGRKPKVEOLSNMIVRSCKS 390
 DB 344 NOHNPASAPCCVPQALEPLIYVYVGRKPKVEOLSNMIVRSCKS 390

RESULT 4
 5168051-2
 Patent No. 5168051
 APPLICANT: DERVICK, RIK M.A.; GOEDEL, DAVID V.
 TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
 NUMBER OF SEQUENCES: 21
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/389, 929
 FILING DATE: 04-AUG-1989
 SEQ ID NO: 2:
 LENGTH: 390
 5168051-2

Query Match 88.9%; Score 1919.5; DB 6; Length 390;
 Best Local Similarity 89.7%; Pred. No. 3e-169;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 DB 1 MPSPGLRLPLPLMLVLTTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 QY 61 SPSPGDVPPGPPEAVLALYNSTRDVAGSEVPEPEPEADYYAKETRVLMVESGNOI 120
 DB 61 SPSPGDVPPGPPEAVLALYNSTRDVAGSEVPEPEPEADYYAKETRVLMVETHEI 120

QY 121 YDKFKGTPHSLYMLFNTSELRVAVPEVLLSRALRLRLKLYEQHVELYQKYSNDSMR 180
 DB 121 YDKFKGTPHSLYMLFNTSELRVAVPEVLLSRALRLRLKLYEQHVELYQKYSNDSMR 180
 QY 181 YLSNRLAPSDSPWLSFDYTGVRQWLSRGEIEGFRLSAHSCSDSDNTLOVDINGFT 240
 DB 181 YLSNRLAPSDSPWLSFDYTGVRQWLSRGEIEGFRLSAHSCSDSDNTLOVDINGFT 240
 QY 241 SGRGDLATIHGMNRPFLMLATPLERAQHLSSRRRALDTSYDYVASYALDTN 300
 DB 241 TGRGDLATIHGMNRPFLMLATPLERAQHLSSRRRALDTSYDYVASYALDTN 283
 QY 301 YCFSTTEKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVLALY 360
 DB 301 YCFSTTEKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVLALY 360
 QY 284 YCFSTTEKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVLALY 343
 DB 284 YCFSTTEKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPPIYMSLDTOYSKVLALY 343
 QY 361 NOHNPASAPCCVPQALEPLIYVYVGRKPKVEOLSNMIVRSCKS 407
 DB 361 NOHNPASAPCCVPQALEPLIYVYVGRKPKVEOLSNMIVRSCKS 390
 QY 344 NOHNPASAPCCVPQALEPLIYVYVGRKPKVEOLSNMIVRSCKS 390
 DB 344 NOHNPASAPCCVPQALEPLIYVYVGRKPKVEOLSNMIVRSCKS 390

RESULT 5
 US-07-669-171-2
 Sequence 2, Application US/07669171
 Patent No. 5304541
 GENERAL INFORMATION:
 APPLICANT: PURCHIO, ANTHONY F.
 APPLICANT: MADISEN, LINDA
 APPLICANT: MERWIN, JUNE RAE
 TITLE OF INVENTION: TGF-b1/b2: A NOVEL CHIMERIC TRANSFORMING
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PENNIE & EDMONDS
 STREET: 1155 AVENUE OF THE AMERICAS
 CITY: NEW YORK
 STATE: N.Y.
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/669,171
 FILING DATE: 19910314
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MISROCK, S. LESLIE
 REGISTRATION NUMBER: 18,972
 REFERENCE/DOCKET NUMBER: 5624-159-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-669-171-2

Query Match 88.7%; Score 1914.5; DB 1; Length 390;
 Best Local Similarity 89.4%; Pred. No. 8.7e-169;
 Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;

QY 1 MAPSGRLPLPLPLMLVLTTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 DB 1 MPSPGLRLPLPLMLVLTTPGRPAAGLSTCKTIDMELVKKRIEIRGOILSKRLA 60
 QY 61 SPSPGDVPPGPPEAVLALYNSTRDVAGSEVPEPEPEADYYAKETRVLMVESGNOI 120
 DB 61 SPSPGDVPPGPPEAVLALYNSTRDVAGSEVPEPEPEADYYAKETRVLMVETHEI 120

88.48; Score 1909; DB 5; Length 394;
89.58; Pred. No. 2.8e-168;

TELEPHONE: 415/222-1888
TELEFAX: 415/952-9881

TELEPHONE: 415/222-1888
TELEFAX: 415/952-9881

; CURRENT FILING DATE: 1999-12-21
 ; PRIOR APPLICATION NUMBER: PCT/CA98/00180
 ; PRIOR FILING DATE: 1998-03-05
 ; PRIOR APPLICATION NUMBER: US 60/039,919
 ; PRIOR FILING DATE: 1997-03-07
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 412
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-380-662-21

Query Match 38.2%; Score 824.5; DB 4; Length 412;
 Best Local Similarity 44.2%; Pred. No. 4.8e-68;
 Matches 188; Conservative 58; Mismatches 126; Indels 53; Gaps 13;

QY 15 LMVLVLTGPRAGAGTCTKIDMELVKRRRIEIRGOILSKRLASPPSGDVPFGPLP 74
 DB 9 LVVLLALNFATVSLSTCTTLDGHIKKRVEAIRGOILSKRLTSPPEPTVMT--HVP 66
 QY 75 EAVLALYNSTR--DRVAGESE--PEPEADYAKETRVLMVE--SGNQIYDKFKG 126
 DB 67 YQVLAALYNSTRLEEMHREGCGTQENTSEYAKETIKHFDIMIOGLAEHNEILAVCPKG 126
 QY 127 TPHSILMFTSELREAVPEPVLLSRBELRLRL--KLKVEQHVELYQKYSND----S 178
 DB 127 ITSKEVR-FNVSSVER--NRTNLFRAEFRLVLPNPSSKRNEQRIELFQILRPDEHIAT 182
 QY 179 WRYLNRLLAPSDSPMELSDVTGYVROWLTLRREALIEGRFLSAH-----SSSDSKDN- 230
 DB 183 QRYIGGKNLPRTGTAEMLSFDVTGYREMLLRRESNLGLEISIHCPCHTQPNQDILIENT 242
 QY 231 --TLHVEINGFNS--GRGDLATIHGM--NRPELLMATPLERAQHLSSRHRLALDT 282
 DB 243 HEVMEIKFKGVNEDDHGDLGRLLKKOKDHNPHILMMIPRHLDNPGOGGRK---- 298
 QY 283 NSPYDVPDYASLADTNYCFSSSTEKNCCVROLYIDFRKDLGKWHIERPGYANFCLGP 342
 DB 299 -----KRALDTNYCFRLNECCVRLYIDFRDLGKWHIERPGYANFCSGP 347
 QY 343 CPYIWSLDTQYSKVLATYNOHNPASAPCCVPOALEPPIYVYUGRKRYEOLSMIYR 402
 DB 348 CPYLRASADTHTSTVGLYNTLNPEASASPCVQDLEPLTILYVGRTRPVQDLSNMVVK 407
 QY 403 SCKCS 407
 DB 408 SCKCS 412

RESULT 10
 PCT-US91-04541-2
 ; Sequence 2, Application PC/TUS9104541
 ; GENERAL INFORMATION:
 ; APPLICANT: Oncogene Science Inc.
 ; TITLE OF INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Cooper & Dunham
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/04541
 ; FILING DATE: 19910625
 ; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 1919/22669-F-PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)977-9550
 ; TELEFAX: (212)664-0525
 ; TELEEX: 42523 COOP UT
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 412 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US91-04541-2

Query Match 38.2%; Score 824.5; DB 5; Length 412;
 Best Local Similarity 44.2%; Pred. No. 4.8e-68;
 Matches 188; Conservative 58; Mismatches 126; Indels 53; Gaps 13;

QY 15 LMVLVLTGPRAGAGTCTKIDMELVKRRRIEIRGOILSKRLASPPSGDVPFGPLP 74
 DB 9 LVVLLALNFATVSLSTCTTLDGHIKKRVEAIRGOILSKRLTSPPEPTVMT--HVP 66
 QY 75 EAVLALYNSTR--DRVAGESE--PEPEADYAKETRVLMVE--SGNQIYDKFKG 126
 DB 67 YQVLAALYNSTRLEEMHREGCGTQENTSEYAKETIKHFDIMIOGLAEHNEILAVCPKG 126
 QY 127 TPHSILMFTSELREAVPEPVLLSRBELRLRL--KLKVEQHVELYQKYSND----S 178
 DB 127 ITSKEVR-FNVSSVER--NRTNLFRAEFRLVLPNPSSKRNEQRIELFQILRPDEHIAT 182
 QY 179 WRYLNRLLAPSDSPMELSDVTGYVROWLTLRREALIEGRFLSAH-----SSSDSKDN- 230
 DB 183 QRYIGGKNLPRTGTAEMLSFDVTGYREMLLRRESNLGLEISIHCPCHTQPNQDILIENT 242
 QY 231 --TLHVEINGFNS--GRGDLATIHGM--NRPELLMATPLERAQHLSSRHRLALDT 282
 DB 243 HEVMEIKFKGVNEDDHGDLGRLLKKOKDHNPHILMMIPRHLDNPGOGGRK---- 298
 QY 283 NSPYDVPDYASLADTNYCFSSSTEKNCCVROLYIDFRKDLGKWHIERPGYANFCLGP 342
 DB 299 -----KRALDTNYCFRLNECCVRLYIDFRDLGKWHIERPGYANFCSGP 347
 QY 343 CPYIWSLDTQYSKVLATYNOHNPASAPCCVPOALEPPIYVYUGRKRYEOLSMIYR 402
 DB 348 CPYLRASADTHTSTVGLYNTLNPEASASPCVQDLEPLTILYVGRTRPVQDLSNMVVK 407
 QY 403 SCKCS 407
 DB 408 SCKCS 412

RESULT 11
 5262319-2
 ; Patent No. 5262319
 ; APPLICANT: IWATA, KENNETH K.; FOULKES, J. GORDON; DIJKE,
 ; PETER T.; HALEY, JOHN D.
 ; TITLE OF INVENTION: METHOD FOR OBTAINING BONE MARROW FREE
 ; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
 ; NUMBER OF SEQUENCES: 9
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/543,341
 ; FILING DATE: 25-JUN-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 353,410
 ; FILING DATE: 17-MAY-1989
 ; APPLICATION NUMBER: 183,410
 ; FILING DATE: 20-APR-1988
 ; APPLICATION NUMBER: 111,022
 ; FILING DATE: 20-OCT-1987
 ; APPLICATION NUMBER: 922,121
 ; FILING DATE: 20-OCT-1986


```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/132.405
FILING DATE: 06-OCT-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/063841
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790856
FILING DATE: 12-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/401906
FILING DATE: 01-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 597D1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-132-405-2

Query Match
Best Local Similarity 43.2%; Score 809; DB 1; Length 414;
Matches 181; Conservative 62; Mismatches 116; Indels 60; Gaps 14;

QY 27 AAGLSTCKTIDMELVKKRIEAIKRGQLSKRLASPPSGDVP--PGPLPEAVLALYNSTR 85
DB 18 ALSTLCSTIDMDQFMKKRIEAIKRGQLSKRLASPPSGDVP--DYPEPEVPEVISIYNSTR 75
QY 86 D---RVAGESYEPPE--PEADYAKAVTVRLM---VESGNOIYDKFGKTPHSLYMLFNT 137
DB 76 DLLOKASRAAACERESDEEYAKVYKIDMPFPFSENAIPPTFY--RPFRIYRFVDV 134
QY 138 SELREAVPEPVILSRDELRLRL---KLKV--EQHVELLYQ---KYSNDSWRVLSNRLLA 188
DB 135 SAMEKNASN---LVKAEFRVFLQNPKARVPEQRIELYLQILSKDLSPTQRYIDSKVK 191
QY 189 PSDSPFWLSFDYTGAVROWMTREATEGFRLSAHSSS-----DSKDNTHVE-- 235
DB 192 TRAGEWLSFDYTDVAVHMHKDRNLGFKTSLHCPCTFPVPSNNYIIPKSELEAFRA 251
QY 236 -INGENSGRRGDLATIHGMNR-----PFLLMATPLERAQHLHSSRRRALDNTNSYPYD 288
DB 252 GIDGTSYTSQDQKTIKSTRKNSGKTPHLLMLLPSYRLSESOQTNRRKR----- 302
QY 289 VPDYASLADNTNVCFSSTKNCVROLYIDFRKDLGKMWIHEPKGYHNFCLGCPPIYMS 348
DB 303 -----ALDAAYCFRNVDNCCLRPLIYIDFKRDLGKMWIHEPKGYHNFCLGCPPIYMS 355
QY 349 LDTOYSKVALALYNQHPGASAPCCVPQALEPLPIYVYVGRKPKVEQLSNMIVRSCCS 407
DB 356 SDTOHSHRVLSLYNTINPEASASPCCVSQDLEPLITLYIGTKTKIEQLSNMIVRSCCS 414

RESULT 14
US-08-395-939A-2
Sequence 2, Application US/08395939A
Patent No. 5604204
GENERAL INFORMATION:
APPLICANT: Ammann, Arthur J.
APPLICANT: Rudman, Christopher G.
TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE
TITLE OF INVENTION: GROWTH
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

```

```

STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,939A
FILING DATE: 27-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/132405
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/063841
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790856
FILING DATE: 12-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/401906
FILING DATE: 1-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P0597D1C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-395-939A-2

Query Match
Best Local Similarity 43.2%; Score 809; DB 1; Length 414;
Matches 181; Conservative 62; Mismatches 116; Indels 60; Gaps 14;

QY 27 AAGLSTCKTIDMELVKKRIEAIKRGQLSKRLASPPSGDVP--PGPLPEAVLALYNSTR 85
DB 18 ALSTLCSTIDMDQFMKKRIEAIKRGQLSKRLASPPSGDVP--DYPEPEVPEVISIYNSTR 75
QY 86 D---RVAGESYEPPE--PEADYAKAVTVRLM---VESGNOIYDKFGKTPHSLYMLFNT 137
DB 76 DLLOKASRAAACERESDEEYAKVYKIDMPFPFSENAIPPTFY--RPFRIYRFVDV 134
QY 138 SELREAVPEPVILSRDELRLRL---KLKV--EQHVELLYQ---KYSNDSWRVLSNRLLA 188
DB 135 SAMEKNASN---LVKAEFRVFLQNPKARVPEQRIELYLQILSKDLSPTQRYIDSKVK 191
QY 189 PSDSPFWLSFDYTGAVROWMTREATEGFRLSAHSSS-----DSKDNTHVE-- 235
DB 192 TRAGEWLSFDYTDVAVHMHKDRNLGFKTSLHCPCTFPVPSNNYIIPKSELEAFRA 251
QY 236 -INGENSGRRGDLATIHGMNR-----PFLLMATPLERAQHLHSSRRRALDNTNSYPYD 288
DB 252 GIDGTSYTSQDQKTIKSTRKNSGKTPHLLMLLPSYRLSESOQTNRRKR----- 302
QY 289 VPDYASLADNTNVCFSSTKNCVROLYIDFRKDLGKMWIHEPKGYHNFCLGCPPIYMS 348
DB 303 -----ALDAAYCFRNVDNCCLRPLIYIDFRKDLGKMWIHEPKGYHNFCLGCPPIYMS 355
QY 349 LDTOYSKVALALYNQHPGASAPCCVPQALEPLPIYVYVGRKPKVEQLSNMIVRSCCS 407
DB 356 SDTOHSHRVLSLYNTINPEASASPCCVSQDLEPLITLYIGTKTKIEQLSNMIVRSCCS 414

```

RESULT 15

PCT-US94-03705-6
Sequence 6, Application PC/TUS9403705

GENERAL INFORMATION:

APPLICANT: Mu-En Lee

APPLICANT: Mark A. Petrella

TITLE OF INVENTION: TRANSFORMING GROWTH

TITLE OF INVENTION: FACTOR- INHIBITS

TITLE OF INVENTION: INDUCIBLE NITRIC OXIDE

TITLE OF INVENTION: SYNTHASE GENE

TITLE OF INVENTION: TRANSCRIPTION

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 50z or 55sx

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/03705

FILING DATE: 5 April 1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Janis K. Fraser

REGISTRATION NUMBER: Reg. No. 34,819

REFERENCE/DOCKET NUMBER: 05433/007001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 414

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

PCT-US94-03705-6

Query Match 37.5%; Score 809; DB 5; Length 414;

Best Local Similarity 43.2%; Pred. No. 1,3e-66;

Matches 181; Conservative 62; Mismatches 116; Indels 60; Gaps 14;

QY 27 AAGLSTCKTIDMLVYKRRIRIEAIRGOILSKRLASPPSGDVP-PGPLPAVLALYNSTR 85
DB 18 ALSLSTCSFLDMDOFKRRKRIEAIIRGOILSKRLKLSPE--DYPEPEVPEVISIYNSTR 75
QY 86 D-----RVAGESVPEPE-PEADYIAKEVTRVLM---VESGNQIYDKFKGTPHSILYMLFNT 137
DB 76 DLLOEKASRRRAACERERDEEYIAKEVYKIDMPPEFSENALPPTFY-RPYFRIVAFDV 134
QY 138 SELREAVPEPVLLSRAELRLRL---LKRV-EQHVLEYQ-----KYSNDSWRKYLNSRLA 188
DB 135 SAMEKNASN--LVKAEFYVFRLOMPKARPEQRIELYLQILKSKDLTSPQRYIDSKVK 191
QY 189 PSDSPFWLSFDYTGVRQWLTRREALTEGFRLSAHSSS-----DSKDNLTIAVE-- 235
DB 192 TRAEGEMLSFQYTDVAHEVHLHKDRNLGFKISLHCCCTFVPVNNYIIPKSELEKRAFA 251
QY 236 -INGFNSGKRGDLATIHGMR-----PFLLMATPLERAQHLHSSRRRALDNTSYPD 288
DB 252 GIDGSTYTSYGDKTKSTKRKNSGKTPHLLMLLPSYRLSQQTNRRKKR----- 302
QY 289 VPDYASLADLTWVCFSSSTBKNCVCVRLYIDFRKDLGWMKIHEPKGYHANFCLGRCPTWIS 348

DB 303 -----ALDAAYCFRNVDNCCLRPLYIDFKRDLGKWKIHEPKGYANFACAGACPILMS 355
QY 349 LDTQYSKVIALVYNQHNPGASAPACVPOALEPLPIYIVYGRKREVDLSMAYRSCSKS 407
DB 356 SDTQHSRVLSLYNTINPEASASPCVSODLEPLIITYIYICKTKRIEOLSMNIVYSCSKS 414

Search completed: April 15, 2003, 12:01:58
Job time : 27 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2003, 11:54:18 ; Search time 88 Seconds
(without alignments)
616.284 Million cell updates/sec

Title: US-10-017-372E-37

Perfect score: 2159
Sequence: 1 MAPSGIRLLPLLLPLMLLV.....GRKPKVQLSNMIVRSCKCS 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_101002: *
2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT: *
3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
4: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT: *
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10: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT: *
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12: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT: *
13: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT: *
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19: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT: *
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21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *
22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT: *
23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT: *
24: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2048.5	94.9	390	23	AAE13596 Porcine transforming
2	1926.5	89.2	390	22	AAM339186 Human polypeptide
3	1919.5	88.9	390	7	AAE61468 PreTGF-beta gene p
4	1919.5	88.9	390	11	AAE04034 Sequence of pre-TG
5	1919.5	88.9	390	11	AAE05258 Human pre-transfor
6	1919.5	88.9	390	12	AAE13813 Human pro-TGF-beta
7	1919.5	88.9	390	16	AAE73596 Human TGF-beta 1 p
8	1919.5	88.9	390	17	AAE90827 pre-transforming g
9	1916.5	88.8	390	23	AAU77101 Human transforming
10	1916.5	88.8	390	23	AAE16943 Human transforming

11	1914.5	88.7	390	13	AAE20124 Sequence of simian
12	1910.5	88.5	390	15	AAE46227 Human pre-TGF-beta
13	1909	88.4	390	16	AAE83054 Transforming growt
14	1908.5	88.4	390	19	AAE78785 Human pre-transfor
15	1907.5	88.4	390	22	AAE84601 Nucleotide sequenc
16	1905	88.2	391	9	AAE81362 Human transforming
17	1904	88.2	434	11	AAE03743 Monkey transformin
18	1883.5	87.2	386	11	AAE05663 Simian transformin
19	1878	87.0	387	11	AAE05664 Simian transformin
20	1867.5	86.5	390	11	AAE05492 Chimeric simian TG
21	1863.5	86.3	390	13	AAE27522 TGF-beta 1/beta 2
22	1844	85.4	389	13	AAE29657 TGF-beta 1. Homo
23	1839	85.2	453	22	AAE40972 Human polypeptide
24	1758.5	81.4	390	13	AAE20126 Sequence of hybrid
25	1757.5	81.4	390	11	AAE05749 Human TGF-beta2 ex
26	1751.5	81.1	390	11	AAE05665 Human transforming
27	1749.5	81.0	390	11	AAE05666 Hybrid transforming
28	1742	80.7	391	10	AAE91900 Sequence encoded b
29	1715	79.4	389	16	AAE79921 Simian-human hybr
30	1300	60.2	278	15	AAE53090 Polypeptide cross-
31	1295	60.0	278	12	AAE12541 Latency associated
32	1169	54.1	290	22	ABG06792 Novel human diagno
33	944	43.7	227	22	ABG20234 Novel human diagno
34	901	41.7	226	22	ABG20233 Amino acid sequenc
35	868.5	40.2	382	21	AAE08358 Frog transforming
36	868.5	40.2	382	23	AAU77105 Pig transforming g
37	832.5	38.6	456	19	AAE78786 Human TGF-beta 3 p
38	828.5	38.4	412	16	AAE73598 Pig TGF-beta-3. S
39	825	38.3	456	15	AAE46228 Transforming Growt
40	824.5	38.2	412	13	AAE20621 Amino acid sequenc
41	824.5	38.2	412	19	AAE80417 Human transforming
42	824.5	38.2	412	23	AAU77103 Human Transforming
43	824.5	38.0	457	11	ABE50765 Human Tumour Endot
44	819.5	37.8	457	11	AAE04080 Polypeptide sequen
45	816	37.8	413	13	AAE22038 Mutant Transformin

ALIGNMENTS

RESULT 1	AAE13596	AAE13596 standard; Protein: 390 AA.
ID	AAE13596;	
AC	AAE13596;	
XX		
DT	26-FEB-2002 (first entry)	
XX		
DE	Porcine transforming growth factor beta 1 (TGF-beta1) mutant.	
XX		
KW	Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy;	
KW	IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive;	
KW	multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;	
KW	diabetes mellitus; sarcoidosis; psoriasis; dermatological; mutant;	
KW	muten.	
XX		
OS	Sus scrofa.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 223	/note= "Wild type Cys substituted with Ser"
FT	Misc-difference 225	/note= "Wild type Cys substituted with Ser"
FT		
XX		
PN	WO200181404-A2.	
XX		
PD	01-NOV-2001.	
XX		
PF	20-APR-2001; 2001WO-US12980.	
XX		
PR	20-APR-2000; 2000US-199014P.	
XX		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	

D	b	121	YDFKSTSHSIYFETSELREAVEPVLSSRAELHLRLKLKVEGHVELLYOKYSNSMR	180
Q	y	181	YLNRLLPADSDSEWLSTDVTGYVROWLITRREALIEGFRLSAHSSSKNTLHVELNGFN	240
D	b	181	YLSNRLIAPSDSEWLSFDVTGVVRWMLSGGEIEGFRLSAHSCDSRDMTLVADINGFT	240
Q	y	241	SGSRGLDATHGNRRPFLLMATPLEBAOHLHSRRHRALDTSNPYDVDPYASLALDTN	300
D	b	241	TGRKGLDATHGNRRPFLLMATPLERAOHLHSRRHR-----ALDTN	283
Q	y	301	YCPSSTEKNCCVOLYIDFRKDLGKKWIEHPKYHANFLCIGPCPYTMSLDTOYSKYVALY	360
D	b	284	YCFSTTEKNCCVOLYIDFRKDLGKKWIHEPKGYHANFLCIGPCPYTMSLDTOYSKYVALY	343
Q	y	361	NQNHPGASAAPCCVPALEPLPTVYYYGRRPKYEQSLNMIVRSCKGS	407
D	b	344	NQNHPGASAAPCCVPALEPLPTVYYYGRRPKYEQLSNMIVRSCKGS	390
 RESULT 3 AAP61468				
ID	AAP61468	standard; Protein; 390 AA.		
AC	AAP61468;			
DT	28-OCT-1991	(first entry)		
DE	PretGF-beta gene product.			
KM	Transforming growth factor beta; cancer; wound healing.			
FH	Key Location/Qualifiers			
FT	Protein 279..390			
PN	EP200341-A.			
PD	10-DEC-1986.			
PE	21-MAR-1986; 86EP-0302112.			
PR	22-MAR-1985; 85US-0715142.			
PR	13-MAR-1987; 87US-0025423.			
PA	(GETH) GENENTECH INC.			
PI	DeSynck RNA;			
DR	WPI; 1986-326875/50.			
DR	N-PSDB; AAN60972.			
PT	TGF-beta prodn. from transformed hosts - useful esp. for treating wounds (J6 2/9/86).			
PS	Disclosure; Fig 1b; 26pp; English.			
CC	The gene product is known to stimulate cell proliferation and inhibit anchorage-dependent growth of a variety of human cancer cell lines, it is esp. useful in treatment of burns and the promotion of surface and internal wound healing. TGF-beta may be expressed from a transformed CHO cell line.			
CC				
CC				
CC				
CC				
SQ	Sequence 390 AA:			
Query Match	88.9%; Score 1919.5; DB 7; Length 390;			
Best Local Similarity	89.7%; Pred. No. 9,9e-160;			
Matches 365;	Conservative 10; Mismatches 15; Indels 17; Gaps 1;			
Qy	1 MAPSGRLPLPLPLPLMLVLTTPGPAPAGLSTCKTIDMELVKRKRIEIRGOILSKRLA 60			
D	1 MPESGRLPLPLPLPLMLVLTTPGPAPAGLSTCKTIDMELVKRKRIEIRGOILSKRLA 60			
Qy	61 SPFGSDVPPGCLPEAVLALYNSTRORVAGESVEPEPEADYVAKEVRYRLMVESGNDI 120			

D	b		61	SPEHQGEVPECPRLPENVLALYNSTRDRVAGSENPPEPEPADYAAKEVTVLAVETHEI	120
O	y		121	YDKFKGTPHSLMYLFNTSELREAVPEPVLLSRDELRLRLKLKVEQHVELYOKYSNDSWR	180
D	b		121	YDKRKQSTHLYTFMFNTSELREAVPEPVLLSRDELRLRLKLKVEQHVELYOKYSNNSWR	180
O	y		181	YLSRRLAPSDSPWLSFDVTGVVROMLTRREALIEGFRLSAHSSSDKWTLHVEINGFN	240
D	b		181	YLSRRLAPSDSPWLSFDVTGVVROMLSNGCELGFRLSAHCSCSBRNDTLOVDINGFT	240
O	y		241	SGRRGDLATIHGMNRPEPLLMATPLERAQHLSRRHRALDTNSYPDYDVASLADTN	300
D	b		241	TGRRGDLATIHGMNRPEPLLMATPLERAQHLSRRHR-----ALDTN	283
O	y		301	YCFSSTEKNCCVOLYYTDFFRKDGWKATIHBPKGYHANFCGLGPCPYIMSLDTQSKYLALY	360
D	b		284	YCFSSSTEKNCCVOLYYTDFFRKDGLKMWIHEPKGHANFCLGPCPYIMSLDTQSKYLALY	343
O	y		361	NQHPGASAAPCCVPQALEPLPIYYYGRRPKYEQLSNMIVRSCKCS	407
D	b		344	NQHPGASAAPCCVPQALEPLPIYYYGRRPKYEQLSNMIVRSCKCS	390
 RESULT 4 AAR04034					
I	D	AAR04034		standard; protein; 390 AA.	
X	X	AAR04034:			
A	C				
X	X				
D	T			31-MAY-1989 (first entry)	
X	X				
D	E			Sequence of pre-TGF-beta 1.	
X	X				
K	M			Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth inhibition.	
X	F				
H					
F				Key	Location/Qualifiers
F	T	CDS			348..500
X	X				
P	N			W06912101-A.	
X	X				
P	D			14-DEC-1989.	
X	X				
P	F			08-JUN-1988;	88WO-USO1945.
X	R			08-JUN-1988;	88WO-UOO1945.
P	A			(GETH) GENENTECH INC.	
X	X				
P	I			Deruyck RM, Goeddel DV;	
X	X				
D	R			WPI: 1990-007474/O1.	
X	X			N-PSDB: AAO02815.	
P	T				
X	X			Nucleotide sequence encoding transforming growth factor beta-3 used as a probe, or to produce TGF beta 3, for inhibiting growth of certain normal and neoplastic cells, eg A549.	
P	S				
X	X			Disclosure; Fig. 2; 61pp; English.	
X	X				
C	C			Sequence is an exon of transforming growth factor-beta 1 (pre-TGF-beta 1) polypeptide and corresponds to AA's 288-338 of mature TGF-beta 1. The nucleic acid encoding second subtype of TGF-beta (TGF-beta 3) is useful as a probe or to produce TGF-beta 3 for inhibition of normal and neoplastic cell growth.	
C	C				
X	X				
S	Q			Sequence	390 AA;
 Query Match					
		Best Local Similarity		88.9%; Score 1919.5;	DB 11; Length 390;
		Matches		355; Conservative	10; Mismatches 15; Indels 17; Gaps 1;


```

QY 1 MAPSGRLRLPLPLPLMLVLTGPRPAAGLSTCKTIDMELVKRRIRIAIRGQILSKRLA 60
D 1 MPPSGRLRLPLPLPLMLVLTGPRPAAGLSTCKTIDMELVKRRIRIAIRGQILSKRLA 60
D 61 SPPSGGVPPGPLEAVLALYNSTRDRVAGESEVPEPEADYIAKEVTRVLMVESGNOI 120
D 61 SPPSGGVPPGPLEAVLALYNSTRDRVAGESEVPEPEADYIAKEVTRVLMVESGNOI 120
QY 121 YDKFKGTPHSLVLMFNSTSELREAVPEPVLLSRALRLRLKLVKEQHVLYOKYSNDSMR 180
D 121 YDKFKGTPHSLVLMFNSTSELREAVPEPVLLSRALRLRLKLVKEQHVLYOKYSNDSMR 180
QY 181 YLSNRLAPSDSEWLSFDVTGVYRQMLTRREAIEGFRLSAHSSSDSKDNLTLYVEINGFN 240
D 181 YLSNRLAPSDSEWLSFDVTGVYRQMLTRREAIEGFRLSAHSSSDSKDNLTLYVEINGFN 240
QY 241 SGRGDLATIHGMNRPFLMATPLERAQHLSSRRRALDNTSYPRDYDVAASLADTN 300
D 241 TGRGDLATIHGMNRPFLMATPLERAQHLSSRRRALDNTSYPRDYDVAASLADTN 300
QY 301 YCFSTERNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLY 360
D 301 YCFSTERNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLY 360
QY 361 NQHNPGASAPCCVPQALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 407
D 361 NQHNPGASAPCCVPQALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 407
QY 344 NQHNPGASAPCCVPQALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 390
D 344 NQHNPGASAPCCVPQALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 5
AAR05258
AAR05258 standard; protein: 390 AA.
AAR05258:
05-AUG-1990 (first entry)
Human pre-transforming growth factor-beta-1 (pre-TGF-beta-1).
Transforming growth factor-beta-1 (TGF-beta-1);
neoplastic cell line inhibition;
EGF-potential anchorage-independent growth.
Homo sapiens.
Key Location/Qualifiers
Peptide 1..278
Protein 279..2011
Domain 8..23
Modified-site 82..84
/Note="hydrophobic domain"
Modified-site 136..138
/Note="potential N-glycosylation site"
Modified-site 176..178
/Note="as above"
Modified-site 277..278
/Note="as above"
Cleavage-site 277..278
/Note="proteolytic cleavage site"
US4866747-A.
12-DEC-1989.
13-MAR-1987; 87US-0025423.
13-MAR-1987; 87US-0025423, US-715142.
(GETH ) GENENTECH INC.
DeGynck RMA, Goeddel DV.
WPI: 1990-051338/07.
N-PSDB; AA093301.

```

```

XX Nucleic acid encoding transforming growth factor-beta -
PT cloned into expression vectors for expression in eukaryotic host
D cells for therapeutic use
D Disclosure; Fig 1b; 28pp; English.
CC Pre-TGF-beta-1 is a polypeptide of 390 amino acids. Post-translational
CC cleavage of the precursor gives rise to the mature TGF-beta monomer.
CC The sequence for human TGF-beta was determined by direct amino acid
CC sequence analysis and by deduction from the TGF-beta cDNA. It is
CC capable of inducing EGF-potential anchorage-independent growth of
CC target cell lines, and/or growth inhibition of neoplastic cell lines. It
CC can be used for treating wounds, eg burns or epidermal ulcers.
XX Sequence 390 AA:
SQ
Query Match 88.9%; Score 1919.5; DB 11; Length 390;
Best Local Similarity 89.7%; Pred. No. 9.9e-160;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;
QY 1 MAPSGRLRLPLPLMLVLTGPRPAAGLSTCKTIDMELVKRRIRIAIRGQILSKRLA 60
D 1 MPPSGRLRLPLPLMLVLTGPRPAAGLSTCKTIDMELVKRRIRIAIRGQILSKRLA 60
QY 61 SPPSGGVPPGPLEAVLALYNSTRDRVAGESEVPEPEADYIAKEVTRVLMVESGNOI 120
D 61 SPPSGGVPPGPLEAVLALYNSTRDRVAGESEVPEPEADYIAKEVTRVLMVESGNOI 120
QY 121 YDKFKGTPHSLVLMFNSTSELREAVPEPVLLSRALRLRLKLVKEQHVLYOKYSNDSMR 180
D 121 YDKFKGTPHSLVLMFNSTSELREAVPEPVLLSRALRLRLKLVKEQHVLYOKYSNDSMR 180
QY 181 YLSNRLAPSDSEWLSFDVTGVYRQMLTRREAIEGFRLSAHSSSDSKDNLTLYVEINGFN 240
D 181 YLSNRLAPSDSEWLSFDVTGVYRQMLTRREAIEGFRLSAHSSSDSKDNLTLYVEINGFN 240
QY 241 SGRGDLATIHGMNRPFLMATPLERAQHLSSRRRALDNTSYPRDYDVAASLADTN 300
D 241 TGRGDLATIHGMNRPFLMATPLERAQHLSSRRRALDNTSYPRDYDVAASLADTN 300
QY 301 YCFSTERNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLY 360
D 301 YCFSTERNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLY 360
QY 361 NQHNPGASAPCCVPQALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 407
D 361 NQHNPGASAPCCVPQALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 407
QY 344 NQHNPGASAPCCVPQALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 390
D 344 NQHNPGASAPCCVPQALEPLPIYVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 6
AAR13813
AAR13813 standard; protein: 390 AA.
AAR13813:
20-NOV-1991 (first entry)
Human pro-TGF-beta 1.
Osteogenetic; tumoricidal.
Homo sapiens.
Key Location/Qualifiers
Peptide 1..29
/Note="signal peptide"
Peptide 30..390
/Note="pro-TGF-beta 1"
Peptide 279..390
/Note="TGF-beta 1"
JF03180192-A.

```

XX 06-AUG-1991.
 PD 07-DEC-1989; 89JP-0318243.
 PF 07-DEC-1989; 89JP-0318243.
 PR (KIRI) KIRIN BREWERY KK.
 PA WPI; 1991-271579/37.
 XX N-PSDB; AAQ13392.
 DR Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by
 XX preparing DNA chain contg. base sequence coding for human
 PT pre-pro-TGF-beta 1, forming expression vector etc.
 PS Claim 1; Fig 1; 16pp; Japanese.
 CC The amino acid sequence codes for human prepro-TGF-beta 1 which
 CC can be produced by recombinant methods, it has osteogenetic and
 CC tumoricidal activity.
 XX
 SQ Sequence 390 AA;
 Query Match 88.9%; Score 1919.5; DB 12; Length 390;
 Best Local Similarity 89.7%; Pred. No. 9.9e-160;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;
 QY 1 MAPSGRLRLPLPLPLMLVLTPGRPAAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
 DB 1 MPFGLRLPLPLPLMLVLTPGRPAAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
 QY 61 SPFGQGVPPGPPLPEAVLALYNSTRDRAVAGESVEPEPEADYAKETVRLVMEGNOI 120
 DB 61 SPFGQGVPPGPPLPEAVLALYNSTRDRAVAGESVEPEPEADYAKETVRLVMEGNOI 120
 QY 121 YDKRKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVQHVHVELYOKYSNDSWR 180
 DB 121 YDKRKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVQHVHVELYOKYSNDSWR 180
 QY 181 YLSNRLAPSDSPPEWLSFDYGVVQWMLTRREAIEGFRLSAHSSSDKNTLHVEINGFN 240
 DB 181 YLSNRLAPSDSPPEWLSFDYGVVQWMLTRREAIEGFRLSAHSSSDKNTLHVEINGFN 240
 QY 241 SGRRGDLATIHGMNRPFLMLATPLERAQHLHSSRRRALDNTSYDYDVAASLADTN 300
 DB 241 TGRRGDLATIHGMNRPFLMLATPLERAQHLHSSRRRALDNTSYDYDVAASLADTN 300
 QY 301 YCFSTERNCCVRLYLIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKYLALY 360
 DB 284 YCFSTERNCCVRLYLIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKYLALY 360
 QY 361 NOHNPASAPCCVPOALEPLPIYVYVGGKPKVEQLSNMIVSCSKS 407
 DB 344 NOHNPASAPCCVPOALEPLPIYVYVGGKPKVEQLSNMIVSCSKS 390
 RESULT 7
 ID AAR73596 standard; Protein; 390 AA.
 AC AAR73596;
 XX 20-DEC-1995 (first entry)
 DE Human TGF-beta 1 protein.
 XX Transforming growth factor-beta; Human TGF-beta protein; TGF-beta 1;
 KW TGF-beta 3; osteogenic cell source; OCS; bone deficiency;
 XX bone-inducing cofactor.
 OS Homo sapiens.

PN US5409896-A.
 PD 25-APR-1995.
 XX 12-NOV-1993; 93US-0401906.
 PF 01-SEP-1989; 89US-0401906.
 PR 12-NOV-1991; 91US-0790856.
 PR 18-MAY-1993; 93US-0063841.
 PR 12-NOV-1993; 93US-0132405.
 PA (GETH) GENENTECH INC.
 XX Ammann AJ, Rudman CG;
 PI WPI; 1995-169610/22.
 DR Compns. for treating skeletal tissue deficiency - comprising
 XX transforming growth factor-beta and an osteogenic cell source in a
 PT carrier
 PS Claim 3; Column 15-18; 19pp; English.
 CC This sequence represents human transforming growth factor-beta 1
 CC (TGF-beta 1). This sequence and the sequence for human TGF-beta 3 (see
 CC AAR73598) are claimed within the scope of the invention. The invention
 CC is a composition consisting of a TGF-beta protein and an osteogenic cell
 CC source (OCS) formulated in an acceptable carrier other than a bone
 CC morphogenic cofactor. This composition can be used for the restoration
 CC of bone deficiency. This provides for the generation of mature bone
 CC only where it is required, without the inclusion of a specific
 CC bone-inducing cofactor. This method can be used with any of the 5 human
 CC TGF-beta's or with TGF-beta from other species.
 XX
 SQ Sequence 390 AA;
 Query Match 88.9%; Score 1919.5; DB 16; Length 390;
 Best Local Similarity 89.7%; Pred. No. 9.9e-160;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;
 QY 1 MAPSGRLRLPLPLPLMLVLTPGRPAAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
 DB 1 MPFGLRLPLPLPLMLVLTPGRPAAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
 QY 61 SPFGQGVPPGPPLPEAVLALYNSTRDRAVAGESVEPEPEADYAKETVRLVMEGNOI 120
 DB 61 SPFGQGVPPGPPLPEAVLALYNSTRDRAVAGESVEPEPEADYAKETVRLVMEGNOI 120
 QY 121 YDKRKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVQHVHVELYOKYSNDSWR 180
 DB 121 YDKRKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVQHVHVELYOKYSNDSWR 180
 QY 181 YLSNRLAPSDSPPEWLSFDYGVVQWMLTRREAIEGFRLSAHSSSDKNTLHVEINGFN 240
 DB 181 YLSNRLAPSDSPPEWLSFDYGVVQWMLTRREAIEGFRLSAHSSSDKNTLHVEINGFN 240
 QY 241 SGRRGDLATIHGMNRPFLMLATPLERAQHLHSSRRRALDNTSYDYDVAASLADTN 300
 DB 241 TGRRGDLATIHGMNRPFLMLATPLERAQHLHSSRRRALDNTSYDYDVAASLADTN 300
 QY 301 YCFSTERNCCVRLYLIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKYLALY 360
 DB 284 YCFSTERNCCVRLYLIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKYLALY 360
 QY 361 NOHNPASAPCCVPOALEPLPIYVYVGGKPKVEQLSNMIVSCSKS 407
 DB 344 NOHNPASAPCCVPOALEPLPIYVYVGGKPKVEQLSNMIVSCSKS 390
 RESULT 8
 ID AAR90827 standard; Protein; 390 AA.
 AC AAR90827
 XX AAR90827

[illegible]

Db	61	SPSOGGEVPEPDLDEAYALALYNSTRDXYAGESABDEPEDEPDYAKVITAVLWEHNEI	120
QY	121	YDKERGFPHSLMYLFNTSELREAVPEVLLSRABELRLRLKLVKEQVHELKYOKYSNDNMR	180
Db	121	YDKERGFPHSLMYLFNTSELREAVPEVLLSRABELRLRLKLVKEQVHELKYOKYSNDNMR	180
QY	181	YLSNRLLAPSSPFWLSFDYGVYKWMQITREALIEGRRLSHSSSDSKDNTLHVEINGFN	240
Db	181	YLSNRLLAPSSPFWLSFDYGVYKWMQITREALIEGRRLSHSSSDSKDNTLHVEINGFN	240
QY	241	SGRRGDLATIHGMNRPELLMATPELERAQHHSRRHRRALDTNNSPYDVPDYASLADTN	300
Db	241	TGRRGDLATIHGMNRPELLMATPELERAQHHSRRHRRALDTNNSPYDVPDYASLADTN	300
QY	301	YCSSTETKNCVROLYIDFRKDLGKWIIEBKGYHANFCLGAPCYIWSLDTQYSKYALAY	360
Db	284	YCSSTETKNCVROLYIDFRKDLGKWIIEBKGYHANFCLGAPCYIWSLDTQYSKYALAY	343
QY	361	NOHHPGASAAPCCVPQALPELPYIYYUGRKPKEQSLNMTIVRSCKS	407
Db	344	NOHHPGASAAPCCVPQALPELPYIYYUGRKPKEQSLNMTIVRSCKS	330

	RESULT 9
ID	AAU77101
XX	AAU77101 standard; Protein; 390 AA.
AC	
XX	AAU77101;
DT	05-JUN-2002 (first entry)
XX	
DE	Human transforming growth factor beta 1 (TGF-beta-1) polypeptide.
XX	
KW	Human; transforming growth factor beta; TGF-beta; insulin production;
KW	Type I diabetes mellitus; pancreatic cell outgrowth; wound healing;
KW	pancreatic duct tissue; ischaemia; stroke; nervous system aging;
KW	neurological condition; neurodegenerative disease; inflammation;
KW	vascular injury; chemical injury; traumatic injury; tumour-induced injury;
KW	amorphotic lateral sclerosis; spinocerebellar degeneration;
XX	immunological disease; multiple sclerosis; TGF-beta-1.
OS	Homo sapiens.
XX	
PN	WO200212336-A2.
XX	
PD	14-FEB-2002.
XX	
PF	09-FEB-2001; 2001WO-US04192.
PR	09-AUG-2000; 2000US-0635368.
XX	
PA	(CURI-) CURIS INC.
XX	
PI	Wang M., Pang K;
XX	
DR	WPI; 2002-257468/30.
PT	Treating a subject with a disorder resulting from insufficient insulin
XX	production, and inducing outgrowth of pancreatic cells, involves using
PS	a transforming growth factor beta therapeutic -
XX	
PS	Disclosure; Fig 1; 77pp; English.
CC	The invention relates to treating a subject with a disorder resulting
CC	from insufficient insulin production, involving contacting the subject
CC	with a transforming growth factor beta (TGF-beta) therapeutic. TGF-beta
CC	polypeptides can be used for treating a subject with a disorder resulting
CC	from insufficient insulin production, e.g. type I diabetes mellitus, and
CC	for inducing outgrowth of pancreatic cells associated with pancreatic
CC	duct tissue within a subject. A composition comprising a TGF-beta protein
CC	may be useful in wound healing and treatment of neurological conditions
CC	derived from acute, subacute or chronic injury to the nervous system,

[illegible]

Pt	oxide synthase gene transcription
Xx	
Ps	Disclosure; Fig 17; 52pp; English.
Cc	
Xx	Transforming growth factor-beta 1 (TGF-beta 1) has been found to inhibit inducible nitric oxide synthase (iNOS) gene transcription, esp. in interleukin-1 beta (IL1-beta) stimulated rat smooth muscle cells, and at a dose which does not inhibit constitutive NOS. TGF-beta 1 or 2 (AAR83055) or their active fragments (esp. derived from the carboxy-terminal 112 amino acids), can be used in the treatment of hypertension, such as that associated with severe inflammation or septic shock.
Cc	
Cc	
Sq	Sequence 391 AA:
Qy	Query Match 88.4%; Score 1909; DB 16; Length 391; Best Local Similarity 89.5%; Pred. No. 8.3e-159;
Matches	365; Conservative 10; Mismatches 13; Indels 18; Gaps 2
Db	1 MAPSGRLRLPLRLPLMLVLTPGPPAGLSTCKTDIMELVYRKRIEALRGILSKRLA 60 1 MPSPGLRLPLRLPLRLMLVLTPGPPAGLSCTKTDIMLVYRKRIEALRGILSKRLA 60
Oy	61 SPPSGGDVPPEGPLPEAVLYALYNSTRDRAAGESVEPEPEPEADYIAKEVTYRLMESGNQI 120 61 SPSSGGEVPPGEPLEPAVALYNSTRDRVAGESAEPEPEPEADYIAKEVTYRLVETHNEI 120
Oy	121 YDKFEGPTSLVCLMNTSRLREAVEPPLLRSARELRLL-RLLKYRQHVELYOKYSNDSM 179 : 121 YDKFOOSTISITIMEFTNSLREAVEPPLLRSARELRLLKLRYKHQLVOKYSNNSM 180
Oy	180 RYLSNRLAPSDSPEMLSFDVGVYROWLTREALEGFRLSAHSSSDSKDNTLHVEINGF 239 181 RYLSNRLLAPSDSPMLSPDVGVYRWQLSRGELIEGFLSHSCDSNDNLQVDINSEF 240
Oy	240 NSGRGGDLATIHGANRPILLMATPLERAQHLHSSRHRRALDTNSTPYDPYASIALDT 299 : 241 TTGRGGDLATIHGNMRPELLMATPLERAQHQSRRH-----ALDT 283
Oy	300 NVCFSSTEKNCCVOLXIDFRKDLGKKWHEPKGYHANRCIGPCPIWSLDPOYSKVLA 359 Db 284 NVCFSSTEKNCCVOLXIDFRKDLGKKWHEPKGYHANCICLPPIWISLDPOYSKVLA 343
Oy	360 YNOHPNGASAAPCPQALDEPLIYYVYGKRKRVQLDSNMIVRSCKCS 407 Db 344 YNOHPNGASAAPCVQALDEPLIYYVYGKRKRVQLDSNMIVRSCKCS 391
Result	14
ID	AAW78785
AC	AAW78785 standard; Protein; 390 AA.
XX	AAW78785;
XX	
DT	21-DEC-1998 (first entry)
XX	
DE	Human pre-transforming growth factor-beta 1.
KW	Transforming growth factor-beta 1; TGF-beta 1; human.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Domain 8..23
FT	Protein 279..390
FT	Modified-site /label= Mat_protein 82..84
FT	Modified-site /note= "Asn is N-glycosylated" 136..138
FT	Modified-site /note= "Asn is N-glycosylated" 176..178
FT	Modified-site /note= "Asn is N-glycosylated"

FT	Cleavage-site	277..278	/note= "Cleavage site for release of TGF-beta 1"
XX			
XX			
XX	US5801231-A.		
XX			
PD	01-SEP-1998.		
XX			
PF			
XX	22-MAR-1985;	85US-0715142.	
PR	13-MAR-1987;	87US-0025423.	
XX			
PR	22-MAR-1985;	85US-0715142.	
PR	04-AUG-1989;	89US-0389929.	
PR	04-MAR-1992;	92US-0845893.	
PR	05-NOV-1993;	93US-0147364.	
PR	30-MAY-1995;	95US-0454468.	
PA			
XX	(GETH) GENENTECH INC.		
PI	Derynck RMA, Goeddel DV;		
XX			
DR	MP1: 1998-494840/42.		
DR	N-PSDB; AAV52933.		
XX			
PT	DNA encoding transforming growth factor-beta precursor sequence -		
PT	useful for analysis to perform manipulations to increase yield of		
PT	recombinant production of the protein		
XX			
PS	Example 3; Fig 1B 1-3; 26pp; English.		
XX			
CC	This is the amino acid sequence of human transforming growth		
CC	factor-beta 1 precursor (preTGF-beta 1). It was deduced from		
CC	a preTGF-beta 1 cDNA sequence (see AAV52933). The invention relates		
CC	to the recombinant production of TGF-beta. Biologically active		
CC	TGF-beta is defined as being capable of inducing EGF-potentiated		
CC	anchorage independent growth of target cell lines and/or growth		
CC	inhibition of neoplastic cell lines. Nucleic acids encoding		
CC	TGF-beta have been isolated and cloned into vectors which are		
CC	replicated in bacteria and expressed in eukaryotic cells. TGF-beta		
CC	recovered from transformed cells is used in known therapeutic		
CC	applications.		
XX			
SO	Sequence 390 AA;		
	Query Match 88.4%; Score 1908.5; DB 19; Length 390;		
	Best Local Similarity 89.2%; Pred. No. 9,1e-159;		
	Matches 363; Conservative 10; Mismatches 17; Indels 17; Gaps		
QY	1 MAFSGRLPLPLPLPLMLVLTPGRPAAGLSTCKTIDMELVKKRKRIAIRGQILSKRLA 60		
DB	1 MPSPGLRLPLPLPLMLLVLPGRPAPELSTCKTIDMEQVKKRKRIAIRGQILSKRLA 60		
QY	61 SPSPQGVPPPLPEAVLALYNSTRDRAVAGESEVEPEPEPADYAAKEVTRVLWESGNOI 120		
DB	61 SPSPQGVPPPLPEAVLALYNSTRDRAVAGESEVEPEPEPADYAAKEVTRVLWETHNEI 120		
QY	121 YDKFKGTPLHSLYMLFNTESELRPAVEPVLLISRAELRLRLKLKVEQVVELYQKTSNDSNR 180		
DB	121 YDKFKQSTHSLYMLFNTESELRPAVEPVLLISRAELRLRLKLKVEQVVELYQKTSNNSMR 180		
QY	181 YLSNRILAPSPPELSPFVTVGVNRQMLTRREAIEGRFLSAHSSSDSKDNTLWHEINGFN 240		
DB	181 YLSNRILAPSPPELSPFVTVGVNRQMLTRRGCTIEGFRLSAHSCSDSRDNTLQYDINGFT 240		
QY	241 SGRGGLATLTHGMNPPFLMLMATPLERAQHLSSRRRLADTNSYPYDVPDYASLADTN 300		
DB	241 TGRGGLATLTHGMNPPFLMLMATPLERAQHLSSRRRLADTNSYPYDVPDYASLADTN 300		
QY	301 YCESSTEKNCCYRQLYIDPRKDLGKMWIHEPKGYHANFCGLGPCYINSLDTQYSKVALY 360		
DB	284 YCFSTSTEKNCCYRQLYIDPRKDLGKMWIHEPKGYHANFCGLGPCYINSLDTQYSKVALY 343		
QY	361 NQHPGASAPCCVQALPEPLPIVYVYVGRPKYEQOLSNNMIVRSCKS 407		

DB	344	NOHNGASAPCCVPGALEPLPIVYVGRKPKVEQJLSNMIVRSCKS	390
		RESULT 15	
XX	AC	AAB84601	
XX	AC	AAB84601 standard; Protein; 390 AA.	
XX	DT	05-SEP-2001 (first entry)	
XX	DE	Nucleotide sequence of transforming growth factor-beta.	
XX	KM	Growth factor; protein inhibitor; protease; damaged tissue;	
KM	KM	platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;	
KM	KM	connective tissue derived growth factor; CTGF; chrysalin; VEGF;	
KM	KM	keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;	
KM	KM	transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;	
KM	KM	granulocyte macrophage colony stimulating factor; GM-CSF; UPA;	
KM	KM	vascular endothelial growth factor; urokinase plasminogen activator;	
KM	KM	dermal ulcer; wound.	
XX	OS	Homo sapiens.	
XX	EH	Key Location/Qualifiers	
FT	FT	Misc-difference 159	
FT	FT	/note= "Arg encoded by AGCAGC"	
FT	FT	Misc-difference 321	
FT	FT	/note= "Cys encoded by TTC"	
FT	FT	Misc-difference 378	
FT	FT	/note= "Glu encoded by CAG"	
XX	PN	WO200149309-A2.	
XX	PD	12-JUL-2001.	
XX	PF	21-DEC-2000, 2000MO-IB01935.	
XX	PR	29-DEC-1999; 99GB-0030768.	
XX	PA	(PF1Z) PRIZER LTD.	
XX	PA	(PF1Z) PRIZER INC.	
XX	PI	Davies MJ, Huggins JP, McIntosh FS, Occleston NL;	
XX	PI	WPI: 2001-418351/44.	
DR	DR	N-PSDB; AAH28216.	
PT	PT	Composition for the treatment of damaged tissue i.e. chronic wounds and	
PT	PT	dermal ulcers comprises an inhibitor agent i.e. a protease and a growth	
XX	XX	factor -	
XX	XX	Disclosure; Page 547; 572pp; English.	
XX	XX	The specification describes a pharmaceutical composition, comprising	
CC	CC	a growth factor, an inhibitor agent, i.e. a protease. The inhibitor	
CC	CC	agent inhibits the action of at least one specific adverse protein,	
CC	CC	i.e. a protease, that is upregulated in a damaged tissue such as a	
CC	CC	wound environment. Growth factors which are included in the composition	
CC	CC	of the invention are platelet-derived growth factor (PDGF), fibroblast	
CC	CC	growth factor (FGF), connective tissue derived growth factor (CTGF),	
CC	CC	keratinocyte-derived growth factor (KGF), transforming growth	
CC	CC	factor-beta (TGF-beta), granulocyte macrophage colony stimulating factor	
CC	CC	(GM-CSF), epidermal growth factor (EGF), vascular endothelial growth	
CC	CC	factor (VEGF), and chrysalin. Inhibitors which are included in the	
CC	CC	composition of the invention include inhibitors of urokinase-type	
CC	CC	plasminogen activator (uPA) and matrix metalloproteinase (MMP). The	
CC	CC	composition is useful for the treatment of chronic damaged tissue, i.e.	
CC	CC	wounds and dermal ulcers. The present sequence represents a human	
CC	CC	TGF-beta, and is used to produce the composition of the invention.	
XX	XX	Sequence 390 AA;	
XX	XX		

Query Match	88.4%;	Score 1907.5;	DB 22;	Length 390;
Best Local Similarity	89.2%;	Pred. No. 1,1e-158;		
Matches 363;	Conservative 11;	Mismatches 16;	Indels 17;	Gaps 1;
QY	1	MAPSGRLRLPLLLPLIMLVLTTPGRPAALSTCKTIDMELVYKRRIEALRGQILSKRLA	60	
Db	1	MPPSGRLRLPLLLPLIMLVLTTPGRPAALSTCKTIDMELVYKRRIEALRGQILSKRLA	60	
QY	61	SPPSGDVPPGLPEAVLALYNSTDNRVAGESVEEPPEEADYIAKEVTRVLAVESGNOI	120	
Db	61	SPPSGDVPPGLPEAVLALYNSTRRAAGESAEPEPEEADYIAKEVTRVLAVETIHEDI	120	
QY	121	YDKFKGTPHSLYMLFNTSELREAVEPEPVLLSRAELRLKTKVQOHVELYOKYSNDSMR	180	
Db	121	YDKFKQSTHSIYMFNTSELREAVEPEPVLLSRAELRLKTKVQOHVELYOKYSNNSMR	180	
QY	181	YLSNLLPAASDSEPMLSFVYGVYQVQMLTRFRAIGSFRLSAHSSSDSKDNTLVAEINGFN	240	
Db	181	YLSNLLPAAVSDSEPMLSFVYGVYQVQVMSLRGEIIGCFRLSAHSCDSDRNTLVQVINGFT	240	
QY	241	SGRRDGLATIHGSMRPFLLMATPLERAQNHLSRRHRRALDNTSYPYDVDPVASLADPTN	300	
Db	241	TGRRDDLATIHGSMRPFLLMATPLERAQNHLSRRHRRALDNTSYPYDVDPVASLADPTN	300	
QY	301	YCESSTEKKCCRCOLYIDFRKDLGSKKATHEPKGYANPLCEGPCPIYMSLDPOYSKVALLY	360	
Db	284	YCESSTEKKCCRCOLYIDFRKDLGSKKATHEPKGYANANCLGCPPIYMSLDPOYSKVALLY	343	
QY	361	NOHNGASAAPCCVPOALEPLPIYVYVYVYGRKRPEQVDSNMVYSKCS 407		
Db	344	NOHNGASAAPCCVPOALEPLPIYVYVYVYGRKRPEVDELSNMVYRSKCS 390		

Search completed: April 15, 2003, 11:58:17
Job time : 91 secs

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 10:08:23 ; Search time 3935 Seconds
(without alignments)
10065.799 Million cell updates/sec

Title: US-10-017-372E-36

Perfect score: 1361

Sequence: 1 tggtaaccgagatgcgcctt.....cgattaagcgcgcgcgact 1361

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 2054640 segs, 14551402878 residues 4109280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rtd:*
36: em_hlg_mam:*
37: em_hlg_vrl:*
38: em_sy:*
39: em_hlg_hum:*
40: em_hlg_mus:*
41: em_hlg_others:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1221.2	89.7	3306	4	PICTFGB1A
2	1211.8	89.0	1326	4	AX338213
3	1201.8	88.3	1750	4	GGTGFBI
4	1131.6	83.1	1605	4	STGFBFBI
5	1110.2	81.6	2221	4	AF461808
6	990.6	72.8	1369	4	DCGTGFBI
7	979.6	72.0	2527	6	E00973
8	978.8	71.9	2537	6	A06669
9	972.8	71.5	1173	4	OMTGFBI
10	972.4	71.4	1780	4	BC000125
11	972.4	71.4	1780	9	BC001180
12	971	71.3	1561	9	AGMTGFB
13	968.2	71.1	1821	6	E03028
14	967.8	71.1	1746	9	BC022242
15	966.6	71.0	1560	6	I06216
16	965.8	71.0	2745	9	HSTGFB1
17	964.6	70.9	1560	6	I08268
18	947.2	69.6	1569	6	I06221
19	942.2	69.2	1561	6	I08275
20	918.4	67.5	1173	4	ECRGFB1
21	916.6	67.3	1176	6	AX481432
22	912	67.0	1187	4	AF175709
23	889.2	65.3	1597	10	AF191297
24	860.8	63.2	1641	10	BC013738
25	847	62.2	1579	10	MUSTGFRNA
26	847	62.2	2094	10	MMU009862
27	827.4	60.8	1585	10	RMTGFB1
28	815.6	59.9	1117	4	BOYTFGB
29	791	58.1	1125	10	AF480858
30	682.2	50.1	1675	6	I03310
31	543.6	39.9	699	6	I05434
32	357.6	26.3	650	9	AX336646
33	357.6	26.3	650	9	HUMTGFBI
34	357.6	26.3	862	6	I03312
35	354.6	26.0	489	6	AX455100
36	327.2	24.0	469	10	NATGFB1
37	318.2	23.4	1256	5	CHRTGFB4
38	310.2	22.8	339	6	AR036686
39	308.6	22.7	339	6	OCFA000133
40	308.6	22.7	339	6	A18277
41	308.6	22.7	339	6	A23751
42	308.6	22.7	339	6	A48549
43	308.6	22.7	339	6	A48563
44	308.6	22.7	339	6	I56854
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ALIGNMENTS

RESULT 1
LOCUS PICTFGB1A
DEFINITION Sus scrofa transforming growth factor beta-1 mRNA, complete cds.
ACCESSION M23703
VERSION M23703.1 GI:755044
KEYWORDS transforming growth factor-beta-1.
SOURCE Sus scrofa (strain miniature swine) CDNA to mRNA.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 3206)
AUTHORS Kondaliah, P., Van Obberghen-Schilling, E., Ludwig, R. L., Dhar, R.,
Sporn, M. B. and Roberts, A. B.
TITLE cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.

FEATURES	Location/Qualifiers
source	1..1326 /organism="Sus scrofa" /db_xref="taxon:9823"
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BASE COUNT	263 a 438 c 392 g 223 t
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Query Match	89.0%; Score 1211.8; DB 6; Length 1326;
Best Local Similarity	95.6%; Pred. No. 1.4e-209;
Matches 1299; Conservative	0; Mismatches 7; Indels 53; Gaps 3;
QY	1 TGTGACCGAGATGCGCGCTTCGGGGCTCGCGCTCTTCGCGCTGCTGCTGCCCTGCTG 60
DB	6 TGTGACCGAGATGCGCGCTTCGGGGCTCGCGCTCTTCGCGCTGCTGCTGCCCTGCTG 65
QY	61 GCTGCTAGTGTGAGAGCGCTGGCGCGCGCGCGCGCGGACTGTCCACTGTCAACATCA 120
DB	66 GCTGCTAGTGTGAGAGCGCTGGCGCGCGCGCGCGCGGACTGTCCACTGTCAACATCA 125
QY	121 CATGAGAGCTGTGAAGCGGAGCGCATGAGGCCATTGCGGGCAGATTCTGTCCAGCT 180
DB	126 CATGAGAGCTGTGAAGCGGAGCGCATGAGGCCATTGCGGGCAGATTCTGTCCAGCT 185
QY	181 TCGGCTGTGCACACCCCCCGGACGAGGGGAGCGGCGCGCGCGCGCTCTGTAGAGCAGT 240
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QY	241 ACTGAGCTCTTTACAACAGTACCACCGCGGAGTGGCGGGGAAAGTGTGAAACCGAGCC 300
DB	246 ACTGAGCTCTTTACAACAGTACCACCGCGGAGTGGCGGGGAAAGTGTGAAACCGAGCC 305
QY	301 CGAGCCAGAGGGGAGCTACTAGCGCCAAAGAGTCAACCGCGTCTATAGGTGGAAGCGG 360
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QY	361 CAACCAAACTATGATTAATTTCAAGGGACACCCGCCACAGCTTATATATGCTGTTCAACAC 420
DB	366 CAACCAAACTATGATTAATTTCAAGGGACACCCGCCACAGCTTATATATGCTGTTCAACAC 425
QY	421 GTGCGAGCTCCGGGAAGCGGTGCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCT 480
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QY	481 GCTGAGGCTCAATTAAATGTGAGAGCAGCAGTGGAGCTATTACAGAAATACAGCAATGA 540
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QY	661 TCGGCTAGAGGCCACACTTCTCTGTGACAGAAAGATTAACACACTCCACGCTGGAATTA 720
DB	666 TCGGCTAGAGGCCACACTTCTCTGTGACAGAAAGATTAACACACTCCACGCTGGAATTA 725
QY	721 CGGGTTCAATTCTGGCGCGCGGGGTGACCTGGCACCAATTCAGGCAATGAACGAGCCCTT 780

Db	726	CGGGTTAAATTCTGGCCGCCGGGGGTGACCTCGGCCACCATTCACGGCATGAACGGGCCCTT	785
Qy	781	CCCTCCTCCTCATGTGGCCACCCCGCTGGAGAGGGCCACACCTCGACAGCTCCGGCACCG	840
Db	786	CCCTGCTCCTCATGTGGCCACCCCGCTGGAGAGGGCCACACCTGTGCAGCGTCCGGCACCG	845
Qy	841	CCGAGCCCTGGATACCAACAGCTACCCATACGAGGTGCCAGACTACATCTCTGGCCCT	900
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Qy	901	GGAAATCAACACTACTGCTTTCAGCTCCACGAGAGAACTGCTGGTGGCGCAGCTCTACAT	960
Db	855	GGATATACCAACTACTGTGCTTCAGCTCCACGGAAMAAGCTGCTGCTGGCGAGCTCTACAT	914
Qy	961	TGACTTCCGGAAGACCTCGGGGCTGGAGTGGATTCATGAACCCCAAGGGCTACATGGCAA	1020
Db	915	TGACTTCCGGAAGACCTCGGGGCTGGAGTGGATTCATGAACCCCAAGGGCTACATGGCAA	974
Qy	1021	TTTCTGCGCTGGGGGCGCTTCCCTACATCTGGAGGCGTGAACACTAGTACAGCAAGTCTT	1080
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Db	1035	GGCTTGTACAAACAGCAACAACCGGGGCGCTGGGGCGGCGCTGCTGGCGCGCAAGGC	1094
Qy	1141	GCTGAGGCGACTGCCCATCGTGTACTACTGTGGGCGCGCAAGGCCAAGGTGGAAGCTGTG	1200
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Qy	1201	CAACATGATCGTGCTTCTCTGCAAGTGCAGCTGAGAGCCCGCGCGCCACAGCCCGCGC	1260
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Qy	1261	CACCGGCGAGGGCCCGGACCCACCCCGCGCGCTCACCGGGGCTGTATTTAAGACATCG	1320
Db	1214	CACCGGCGAGGGCCCGGACCCCGCGCGCTCACCGGGGCTGTATTTAAGACATCG	1273
Qy	1321	TGCCCCAGCCCACTTGGATGATTAAGGCGGCGGCCA	1359
Db	1274	TGCCCCAGGCCAC- TGGGATGATTAAGGTGAGAGA	1311
RESULT 3			
LOCUS	GGTGFBI	1750 bp	linear MAM 27-MAR-1996
DEFINITION	Porcine mRNA for transforming growth factor-beta 1.		
ACCESSION	X12373		
VERSION	X12373.1	GI:63808	
KEYWORDS	transforming growth factor-beta 1.		
SOURCE	pig.		
ORGANISM	Sus scrofa		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Bukariyota; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
TITLE	1 (bases 1 to 1750)		
JOURNAL	Jakowlew, S.B.		
	Direct Submission		
	Submitted (14-JUN-1988) Jakowlew S.B., National Institute of		
	health, National Cancer Institute, Laboratory of Chemoprevention,		
	Building 41, Room B902, Bethesda, Maryland 20892, USA		
	2 (bases 1 to 1750)		
	Jakowlew, S.B., Dillard, P.J., Sporn, M.B. and Roberts, A.B.		
	Nucleotide sequence of chicken transforming growth factor-beta 1		
	(TGF-beta 1)		
	Nucleic Acids Res. 16 (17), 8730 (1988)		
JOURNAL	88335639		
MEDLINE	3166520		
PUBMED			
COMMENT	The submitters believe that the chicken cDNA library was		
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	porcine TGF-beta-1. 27-MAR-1996.		
	location/Qualifiers		
	1..1750		
FEATURES	/organism="Sus scrofa"		
source			


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Query Match 81.6%; Score 1110.2; DB 4; Length 2221;
Best Local Similarity 95.2%; Pred. No. 3.2e-191;
Matches 1176; Conservative 0; Mismatches 8; Indels 51; Gaps 1;
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QY 191 AGCCCGCGGAGCGCGAGGCGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 250
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Db 421 CCGGAGACGGGTGCGGAGACTGATATGCTCTCTCGGGCAGAGCTGGCGCTGAGAGCTC 480
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Db 481 AAGTTAAAGTGGAGCAGCAGCTGAGCTATACCAAGAAATACAGCAATGATTCCTGGCGC 540
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QY 731 TCTGGCGCGCGGGGTGACTGCGCCACATTCAGCGGATTAACCGGCTTCTGCTCCTC 790
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QY 851 GATACCACAGCTACCCATACAGAGTGCAGACTACGATCTGCGCCCTGATACCAAC 910
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RESULT 6
DOGTGFB1A
LOCUS 1369 bp mRNA linear MAM 30-Oct-1994
DEFINITION Canine transforming growth factor-beta 1 (TGFB1) mRNA, complete cds.
ACCESSION L34956
VERSION L34956.1 GI:516071
KEYWORDS homologue; transforming growth factor-beta 1;
SOURCE Canis familiaris adult jugular vein endothelial CDNA to mRNA.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 1369)
AUTHORS Manning, A.M., Auchampach, J.A., Drono, R.F. and Slightom, J.L.
TITLE Cloning of a canine CDNA homologous to human transforming growth
factor-beta 1 (TGFBeta1)
JOURNAL Unpublished (1994)
FEATURES
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location/Qualifiers
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FEATURES	Location/Qualifiers
SOURCE	1. .2527 /organism="Homo sapiens" /db_xref="taxon:9606"
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ORIGIN	
Query Match	72.0%: Score 979 6; DB 6; Length 2527;
Best Local Similarity	85.0%: Pred. No.1.4e-167;
Matches 1142:	Conservative 0; Mismatches 149; Indels 53; Gaps 2;
QY	6 CCGAGATGCGCCCTTTCGGGGGCTGCGGCTCTTGCACGCTGCTGCTGCCGCTGCTGTGGCTGC 65
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QY	66 TAGTGTACCGCTTGGCGCGCGCGCGCGCGGACTTCCACTGCAAGACATCGACATGG 125
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QY	186 TTGCCAGCCCCCGAGCCAGGGGGAGCTGGCCGCCCGCGCTGCTGAAGCGATGACTGG 245
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QY	246 CTCCTTTACACAGTATCCCGCGCGCGGGTATGCGCGGGGAAGTGTGCAACCGGAGCCCGAGC 305
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QY	306 CAGAGCGCGACTACTACGCGCAAGAGAGTTCACCGCGTCTATATGTTGGTGAAGACCGCAAC 365
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QY	846 CCGTGAATACCAACAGCTAACCCATACGACGTGCCAGACTAAGCAATCTGCGCGCTGGAGTA 905
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Dd	2104	CAAGCCCATCTTGATGATGATTTAAA	2127		
RESULT 8	A06669	2537 bp	mRNA	linear	PAT 29-JUL-1993
LOCUS	A06669	Synthetic mRNA for prengF-beta1.			
DEFINITION	A06669	GI:412940			
VERSION	A06669.1				
KEYWORDS	.				
SOURCE	synthetic construct.				
ORGANISM	synthetic construct				
FEATURES	artificial sequences.				
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CDS	1..2537				
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ORIGIN					
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Best Local Similarity	84.8%;	Pred. No. 1.9e-167;			
Matches 1146; Conservative	0;	Mismatches 147;	Indels 59;	Gaps 2;	
Oy	6	CCGAGATGGCGCCTTCGGGGCTGGGCTGTTCGCGCTGCTGCGCGCTGTGGCTGC	65		
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Oy	66	TGATGCTGACGCTGGCGCGCGCGCGCGGACGTGCCACTGCAAGACATGCACATGG	125		
Dd	897	TGTGCTGAGAGCCTGGCGCGCGCGCGGACACTATCCACTGCAAGAGTATGCACATGG	956		

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 QY 246 CTCTTTTAAAGATTAACCGGAGCCGCGGAGTTCGAGCCGAGCGCGAGC 305
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 QY 606 ATGTACACCGAGTGTGTGCGGAGTGTGCTGAGCCGAGAGAGGCTATAGAGGTTTTCGCC 665
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 QY 666 TCAAGTGTGCGGAGTGTGTGCGGAGTGTGCTGAGCCGAGAGAGGCTATAGAGGTTTTCGCC 725
 DB 1497 TCAAGTGTGCGGAGTGTGTGCGGAGTGTGCTGAGCCGAGAGAGGCTATAGAGGTTTTCGCC 1556
 QY 726 TCAAGTGTGCGGAGTGTGTGCGGAGTGTGCTGAGCCGAGAGAGGCTATAGAGGTTTTCGCC 785
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DB 1986 TGATGTGGGTTCTGCAAGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 2045
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 DB 2106 CCTGTGCG 2137
 RESULT 9
 OATGFB1
 LOCUS 1173 bp mRNA linear MAM 18-APR-1995
 DEFINITION O.aries mRNA for transforming growth factor-beta 1.
 ACCESSION X76916.1 GI:496648
 VERSION TGF-beta 1; transforming growth factor-beta 1.
 KEYWORDS Ovis aries.
 SOURCE Ovis aries
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprine; Ovis.
 REFERENCE 1 (bases 1 to 1173)
 WOODALL, C.J., MCLAREN, L.J. and WATT, N.J.
 Sequence and chromosomal localisation of the gene encoding ovine latent transforming growth factor-beta 1
 Gene 150 (2), 371-373 (1994)
 JOURNAL MEDLINE 95121932
 PUBMED 7821809
 REFERENCE 2 (bases 1 to 1173)
 WOODALL, C.
 Direct Submission
 AUTHORS Submitted (24-DEC-1993) C. Woodall, Univ. of Edinburgh, Dept. of Veterinary Pathology, Sc. of Vet. Studies, Univ. of Edinburgh, Edinburgh EH9 1QH, UK
 JOURNAL Location/Qualifiers
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 Best Local Similarity 88.7%; Pred. No. 2.5e-166;
 Matches 1086; Conservative 0; Mismatches 87; Indels 51; Gaps 1;
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 QY 71 CTGAGCGCTTGGCGCGCGCGCGCGGAGCTGTCCACCTGCAAGACCATGCAATGAGAGCTG 130
 DB 61 CTGAGCGCTTGGCGCGCGCGCGCGGAGCTGTCCACCTGCAAGACCATGCAATGAGAGCTG 120
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Db 121 GTGAAGCGGAGGCGATCGAGCCATCCGGGTGATTTTGTCCAAACTTCGGCTCCG 180
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OY 251 TACACAGACAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 310
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OY 311 GCGGACTACTAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 370
Db 301 GCGGACTACTAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
OY 371 TATGATTAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 430
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OY 431 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 490
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OY 551 TACCTTACAGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 610
Db 541 TACCTTACAGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
OY 611 ACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 670
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OY 671 GCCCAGCTTCTCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 730
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OY 731 TCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 790
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OY 791 ATGGCAGCCCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 850
Db 781 ATGGCAGCCCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 834
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Db 835 -----GCCCTGAGACACCAAC 849
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Db 1090 CTGCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1149
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RESULT 10
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LOCUS
DEFINITION
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MGC:3119 IMAGE:3351664, mRNA, complete cds.
ACCESSION
BC000125
VERSION
BC000125.1 GI:12652748
KEYWORDS
MGC.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1780)
REFERENCE
Strausberg, R.
Direct Submission
Submitted (03-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
Info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Mess, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Saeedi, Jacqueline
Schell, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stolt,
Michael Thorne, Miranada Tsai, Natasha van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAL Plate: 6 Row: e Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency OR
analysis.
FEATURES
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location/Qualifiers
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RRALDTNCFSESTERNCCVROLYIDFKDLGKWIHEPKGYHANFCLGCPYIMSLDT
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BASE COUNT
341 a 648 c 493 g 298 t
ORIGIN
Query Match 71.4%; Score 972.4; DB 9; Length 1780;
Best Local Similarity 84.5%; Pred. No. 2,9e-166;
Matches 1142; Conservative 0; Mismatches 151; Indels 59; Gaps 2;

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RESULT 11

BC001180

LOCUS BC001180 1780 bp mRNA linear PRI 12-JUL-2001

DEFINITION Homo sapiens, similar to transforming growth factor, beta 1, clone

ACCSSION MGC:2323 IMAGE:335605, mRNA, complete cds.

VERSION BC001180.1 GI:12654682

KEYWORDS MGC.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE 1 (bases 1 to 1780)

JOURNAL Strausberg, R.

Direct Submission

Submitted (11-DEC-2000) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

REMARK Contact: MGC help desk

COMMENT Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin laboratory

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@cgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,

Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,

Leticia Hsiao, Martin Kizyewski, Keta Kutsche, Oliver Lee, Soo

Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven

Ness, Pawan Pandoh, Anna-Liisa Prabu, Parvaneh Seedei, Jacqueline

Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Stolt,

Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy,

George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 6 Row: e Column: 10

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 37097.

Location/Qualifiers

1..1780

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/note="Vector: pOTB7"

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Db	1416	TCCGCAAGAGACCTTGAGGCTGGAGTAGTGATTCACAGAGCCCAAGGGCTACATGCCAATTCT	1475
OY	1026	GCCCTGGGGCCCCCTGCTCCCTACATCTGGAGGCCCTAGACACTCATGACAGCAAGGTCCTGGCTC	1085
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OY	1086	TGTAACAACACAGCACAAACCCGGGGCGGTGGCGGGCGGCCTGTCCTGGTCCCGAGGCGCTGG	1145
Db	1536	TGTATCAACAACAGCAATAACCCGGGGCGGTCTGGCGGGCGGCCTGTCCTGGTCCCGAGGCGCTGG	1595
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Db	1596	AGCCGCTGGCCCCATGCTGTACTACGTGGGGCCGCAAGCCCAAGGTGGAGACAGCTGTCCAACA	1655
OY	1206	TGATCTGTGGCTGCTCTGCAAGTGCACCTGAGGGCCCCCGGCCACAGCCCCCGGCCAACCC	1265
Db	1656	TGATCTGTGGCTGCTCTGCAAGTGCACCTGAGGTCCGGCCCCCGGCCCGGCCCGCCGAG	1715
OY	1266	GGCAGAGCCCCGGCCCCACCCCGCGCCCT-----CACCGGGGCTGTATTTAAGACA	1317
Db	1716	GGCCGGCCCCACCCCGGCCCGCGCCCTGCTTCCCATGTAGGGGCTGTATTTAAGACA	1775
OY	1318	TCGTGCCCCCAAGCCC	1332
Db	1776	CGGTGCCCCCAAGCC	1790
RESULT 14			
LOCUS	BC022242	1746 bp	mRNA linear PRI 04-FEB-2002
DEFINITION	Homo sapiens, clone MGC:22008 IMAGE:4399762,	mRNA, complete cds.	
ACCESSION	BC022242		
VERSION	BC022242.1	GI:18490115	
KEYWORDS	MGC.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 1746)		
JOURNAL	Strausberg, R. Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov		
COMMENT	Contact: MGC help desk Email: cgaabs-f@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www.shgc.stanford.edu Contact: (Dickson, Mark) mcd@panix1.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.		

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Series: IRK Plate: 27 Row: e Column: 21 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

Location/Qualifiers
1..1746

100

Downloaded from <http://ajphaphysocpharm.sagepub.com/> at 11:01 11 November 2014

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XX      10-DEC-1986.
XX      21-MAR-1986; 86EP-0302112.
XX      22-MAR-1985; 85US-0715142.
XX      13-MAR-1987; 87US-0025423.
XX      (GETH ) GENENTECH INC.
XX      Derynck RMA;
XX      WPI: 1986-326875/50.
XX      P-PSDB: AAP61468.
XX      TGF-beta Prodn. from transformed hosts - useful esp. for treating
XX      wounds (J6 2/9/86).
XX      Disclosure: Fig 1b; 26pp; English.
XX      The gene product is known to stimulate cell proliferation and
XX      inhibit anchorage-dependent growth of a variety of human cancer cell
XX      lines, it is esp. useful in treatment of burns and the promotion of
XX      surface and internal wound healing. TGF-beta may be expressed from a
XX      transformed CHO cell line.
XX      Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
XX
Query Match      71.9%; Score 978.8; DB 7; Length 2537;
Best Local Similarity 84.8%; Pred. No. 5e-188;
Matches 1146; Conservative 0; Mismatches 147; Indels 59; Gaps 2;

```

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QY      546 GCGGCTACCTCAGCAACCGGCTGTGCGCCCGCAGTGAATCACCAGAGTGTCTCTTTC 605
DB      1377 GGGATFACCTCAGCAACCGGCTGTGCGCCCGCAGTGAATCACCAGAGTGTCTCTTTC 1436
QY      606 ATGTACCGGAGTGTGCGGCGAGTGTGCTGACCCGACAGAGAGCTATAGAGGTTTTCGCC 665
DB      1437 ATGTACCGGAGTGTGCGGCGAGTGTGCTGACCCGACAGAGAGCTATAGAGGTTTTCGCC 1496
QY      666 TCAGTGGCCACCTCTCTCTGACAGCAAGATATACACACTCCACGAGGGAATTAAGGGGT 725
DB      1497 TTAGCGCCCACTGCTCTCTGACAGCAAGATATACACACTCCACGAGGGAATTAAGGGGT 1556
QY      726 TCAATTCTGGCCCGCGGGGTGACTGTGCGCCACCAATTCACGAGCATGAACCGGCTTCCTGC 785
DB      1557 TCACCTACCGGCGCGCGAGGTGACCTGTGCGCCACCAATTCATGAGCATGAACCGGCTTCCTGC 1616
QY      786 TCCTCATGGCCACCGCGCTGTGAGAGGGCCGACACCTGTGACAGCTCTCCGACCGCCGAG 845
DB      1617 TTCTCATGGCCACCGCGCTGTGAGAGGGCCGACACCTGTGACAGCTCTCCGACCGCCGAG 1675
QY      846 CCCTGATACCAACAGCTACCAATACAGCTGTGCGCCACAGCTACGATCTGTGCGCTTGATA 905
DB      1676 -----GCCCTGGACA 1685
QY      906 CCAACTACTGCTTTCAGCTCCACGAGAGAAAGTGTGCTGTGCGGACGCTCTACATTGACT 965
DB      1686 CCAATTATTTGCTTTCAGCTCCACGAGAGAAAGTGTGCTGTGCGGACGCTGTACATTGACT 1745
QY      966 TCCGGAAGAGACCTGGGCTGTGAGAGTGGATTCAAGAACCCAGAGGCTTACATGCCAATTCT 1025
DB      1746 TCCGGAAGAGACCTGGGCTGTGAGAGTGGATTCAAGAACCCAGAGGCTTACATGCCAATTCT 1805
QY      1026 GCGTGGGCGCCCTGCTCCATCATCTGTGAGGCTGTGAGACCTGATCAGTACAGCAAGTCTGTGCTC 1085
DB      1806 GCGTGGGCGCCCTGCTCCATCATCTGTGAGGCTGTGAGACCTGATCAGTACAGCAAGTCTGTGCTC 1865
QY      1086 TGTACACCAAGCAACACCGGCGGTGCGGCGCGCTGTGCTGTGCGGACGCGCTGTG 1145
DB      1866 TGTACACCAAGCAACACCGGCGGTGCGGCGCGCTGTGCTGTGCGGACGCGCTGTG 1925
QY      1146 AGCCACTGCTTCTGCTGATCTACGTGTGCGGCGCGCAAGGCCAAGTGTGAGAGCTGTCCAAACA 1205
DB      1926 AGCCACTGCTTCTGCTGATCTACGTGTGCGGCGCGCAAGGCCAAGTGTGAGAGCTGTCCAAACA 1985
QY      1206 TGATGTGCTGCTTCTGCAAGTGTGAGGCGCGCGCCGACAGAGCGCCGACCCGACCC 1265
DB      1986 TGATGTGCTGCTTCTGCAAGTGTGAGGCGCGCGCCGACAGAGCGCCGACCCGACCC 2045
QY      1266 GGCAGGCGCGCGCCGACCCGCGCGCT-----CACCGGGCTGTATTTAAGGACA 1317
DB      2046 GGCAGGCGCGCGCCGACCCGCGCGCTGCCCTGTGCGCATGGGGCTGTATTTAAGGACA 2105
QY      1318 TCGTGGCCCAAGCCGACTGTGGATGATTA 1349
DB      2106 CCGTGGCCCAAGCCGACTGTGGGGCCCATTA 2137

RESULT 3
ID      AA003301
ID      AA003301 standard; DNA; 2537 BP.
XX      AA003301;
XX      DT 05-AUG-1990 (first entry)
XX      DE cDNA encoding human pre-transforming growth factor-beta-1 (pre-TGF-beta-
XX      1).
XX      KW Transforming growth factor-beta-1 (TGF-beta-1);
XX      KW neoplastic cell line inhibition;
XX      KW EGF-potential anchorage-independent growth;
XX      OS Homo sapiens.

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XX	Key	location/Qualifiers
FT	CDS	842..2014
FT		/*tag= a
FT	mat_peptide	1676..2011
FT		/*tag= b
FT	misc_difference	37..113
FT		/*tag= c
FT	misc_feature	/note="stable hairpin loops"
FT		2015..2100
FT		/*tag= d
FT		/note="G-C rich sequence
FT		and a downstream TATA-like sequence"
XX		
PD		US4886747-A.
XX		
XX		12-DEC-1989.
XX		
PF		13-MAR-1987; 87US-0025423.
XX		
XX		13-MAR-1987; 87US-0025423.
PR		(GETH) GENENTECH INC.
XX		
PA		Derynck RMA, Goeddel DV;
XX		
PI		WPI: 1990-051338/07 .
DR		P-PSDB; AAR05258.
XX		
PT		Nucleic acid encoding transforming growth factor-beta -
PT		cloned into expression vectors for expression in eukaryotic host
XX		cells for therapeutic use
XX		
PS		Disclosure; Fig 1b; 28pp; English.
XX		
CC		It was obtained by an analysis of several overlapping cDNAs and gene
CC		fragments, leading to the detn. of a continuous sequence corresp. to the
CC		TGF-beta-1 precursor mRNA. It is useful in constructing vectors that
CC		encode biologically active transforming growth factor (TGF-beta),
CC		operably linked to DNA that encodes a secretory leader (SL). It, or a
CC		nucleic acid capable of hybridizing with it, can also be labelled and
CC		used in diagnostic assays for DNA or mRNA encoding TGF-beta or related
CC		proteins.
XX		
SO		Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
	Query Match	71.9%; Score 978.8; DB 11; Length 2537;
	Best local Similarity	84.8%; Pred. No. 5e-188;
	Matches 1146; Conservative	0; Mismatches 147; Indels 59; Gaps
QY	6	CCGAGATGGCGCCCTTGGGGGCGTGGGGCTTTGGCCCTGCTGCTGCCGCTGCTGGCTGC 65
DB	837	CCCCCATGGCCGCGCTCCGCGGCTGCGGCTGCGCGCTGCTACCGCTGCTGGCTAC 896
QY	66	TAGTGTGACGCTGGCGCGCGCGCGCGGACTGTCCACCTGCAAGACATGCATGG 125
DB	897	TGGTGTGACGCGCTGGCGCGCGCGCGCGGACTATTCACCTGCAAGACTATGCATGG 956
QY	126	AGCTGTGACGCGGAGCGCATGAGGCCATTTCGCGGCGAGATTCTGTCAAGCTTGGC 185
DB	957	AGCTGTGACGCGGAGCGCATGAGGCCATTTCGCGGCGAGATTCTGTCAAGCTTGGC 1016
QY	186	TTGGCAGGCGCGCGCGAGGAGGAGTCCGCGCGCGCGCGCGCTGCGCGAGGACAGTACGG 245
DB	1017	TTCGCGAGCGCGCGCGAGGAGGAGTCCGCGCGCGCGCGCGCTGCGCGAGGACAGTACGG 1076
QY	246	CTCTTTACACAGTACCCGCGACCGGGTAGCCGGGAAATGTGTGAACCGGAGCCCGAGC 305
DB	1077	CCCTGTACACAGCACCAGCGACCGGGTAGCCGGGAAATGTGTGAACCGGAGCCCGAGC 1136
QY	306	CAGAGCGGAGTACTACGCCCAAGGAGGTACCCCGCTGTCTAATGTGTGAAGCGGCATCC 365
DB	1137	CTAGAGCGGAGTACTACGCCCAAGGAGGTACCCCGCTGTCTAATGTGTGAAGCGGCATCC 1196

QY	366	AAACGATGTAATTAATTCAGAGGCAACCCCAACAGCTTAATATATGCTTCAACACGCGG	425
Db	1197	AAATCTATGCAAGTTTACAGAGATACACAGATATATATGTTCTTCAACACATCAG	1256
QY	426	AGCTCCGGGAAGGGTCCCGAACCTGTATTGCTCTCTTGGGCAGAGCTCGCGCTGTGA	485
Db	1257	AGCTCCGAGAAGGGGTACCTGACACCCGTTGCTCTCCCGGGGACAGCTCGTCTGTGA	1316
QY	486	GGCTCAAGTTAAAGTGGAGCAGCAGCTGGAGCTATACAGAAATACAGCAATGATTCTT	545
Db	1317	GGCTCAAGTTAAAGTGGAGCAGCAGCTGGAGCTATACAGAAATACAGCAATGATTCTT	1376
QY	546	GGGGCTAACCTCAGAACCGGCTGCTGGGCCCCAGTAGACTCACCGAGGTGGGCTGCTTTG	605
Db	1377	GGGGATACCTCAGAACCGGCTGCTGGGACCACCGAGACTCGCAGAGTGTATTCTTTTG	1436
QY	606	ATGTCAACGGAGTTGTGCGGCAGTGGCTGACCCGACAGAGAGGCTATAGAGGTTTTCGCC	665
Db	1437	ATGTCAACGGAGTTGTGCGGCAGTGGTGTAGCCGCTGAGAGGGGAATTTGAGCGCTTTCGCC	1496
QY	666	TCAGTGGCCCACTCTTCTCTCTGACAGCAAAAGATTAACACACTCCACGTTGGAAATTACGGGT	725
Db	1497	TTTAGCGCCACTGCTCTCTGTGACAGCAGAGGATTAACACACTGCAAGTGAAATCAACGGGT	1556
QY	726	TCATTTCTGACCGCGGGGTGACCTGGCGCACCATTTACAGGATGAACCGGCTTCTCTGC	785
Db	1557	TCACTACCGGCGCGGAGGTACCTGCGCACCATTTATGGATGAACCGGCTTCTCTGC	1616
QY	786	TCCTCATGSGCCACCCGCTGGAGAGGGCCACACCTGCACAGCTCCCGGACCGCGGAG	845
Db	1617	TTTCATATGGCCACCCCGCTGGAGAGGGCCACACATCTGCAGAAAGCTCCCGGACCGCGGA	1675
QY	846	CCCTGGATTACCAACGATACCATATGCAAGTGGCCAGACTACGATCTTGCCCTGGATA	905
Db	1676	-----GCCCTGGACA	1685
QY	906	CCAACTACTGCTTTCAGTCTCAACGAGAAAGAACTGCTGCTGGGCAAGCTTACATTGACT	965
Db	1686	CCAACTACTGCTTTCAGTCTCAACGAGAAAGAACTGCTGCTGGGCAAGCTTACATTGACT	1745
QY	966	TCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCCAAGGCTTACATGCAATTTCT	1025
Db	1746	TCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCCAAGGCTTACATGCAATTTCT	1805
QY	1026	GCGTGGGGCCCTGTCCTACATCTGGAGGCTTGACACTAGTACAGCAAGGCTCCCTGGCTC	1085
Db	1806	GCGTGGGGCCCTGTCCTACATCTGGAGGCTTGACACTAGTACAGCAAGGCTCCCTGGCTC	1865
QY	1086	TGTACCAACAGCACACCCGCGGCGCTGCGGCGGCGGCTGTGACGTGCCAGGCGCTGG	1145
Db	1866	TGTACCAACAGCATATACCCGCGGCGCTGCGGCGGCGGCTGTGACGTGCCAGGCGCTGG	1925
QY	1146	AGCCACTGCCCCATGTGTACTACTGTGGGCGCGCACAGCCCAAGTGGAGAGACTGTCCACA	1205
Db	1926	AGCCACTGCCCCATGTGTACTACTGTGGGCGCGCACAGCCCAAGTGGAGAGACTGTCCACA	1985
QY	1206	TGATTCGTGGCTTCTTGGCAAGTGCAGCTGAGGCGCGCGCCGACAGAGCCCGGCGCACCC	1265
Db	1986	TGATTCGTGGCTTCTTGGCAAGTGCAGCTGAGGCGCGCGCCGACAGAGCCCGGCGCGAG	2045
QY	1266	GGCAGAGCGCGCCACCCCGCGCGCT-----CACCGGGGCTGTATTTAAGGACA	1317
Db	2046	GGCAGAGCGCGCCACCCCGCGCGCTGGCCATGAGGGGCTGTATTTAAGGACA	2105
QY	1318	TCGTGCCCCAAGCCCACTTGGGATGATTTAA	1349
Db	2106	CCGTGCCCCAAGCCCACTTGGGATGATTTAA	2137


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OY 1206 TGATCGTGCCTTCCTGCAGAGCTGAGGCCCCCGCCACAGCCCGCCACC 1265
DB 1986 TGAATCGTGCCTTCCTGCAGAGCTGAGTCCCCCGCCCGCCCGCCAG 2045
OY 1266 GGCAGGCGCGGCCCCACCCCGCCGCT-----CACCGGCGCTGATTTAAGACA 1317
DB 2046 GCCCGGCGCCACCCCGCCCGCCGCTGCTGCTGATGGGCGTGTATTAAAGACA 2105
OY 1318 TCGTGGCCCCAAGCCCACTGGGATCGATTAA 1349
DB 2106 CCGTGCCTCCAGCCCACTGGGCGCCCATTTAA 2137

RESULT 5
AAT15720
ID AAT15720 standard; cDNA; 2537 BP.
AC AAT15720;
XX 24-JUL-1997 (revised)
DT 25-JAN-1980 (first entry)
XX
DE Pre-transforming growth factor beta 1 cDNA.
KW transforming growth factor beta 1; wound healing;
KW recombinant production; ss.
XX Homo sapiens.
FH Key 1 location/Qualifiers
FT 5'UTR 1..841
FT misc-feature 37..113
FT /tag= b
FT /note= "GC-rich region forms stable hairpin loops;
FT similar to structural organisation of c-myc RNA,
FT could play role in mRNA stability or in
FT regulation of transcription"
FT CDS 842..2014
FT /tag= c
FT /product= pre-TGF_beta_1
FT /tag= d
FT /product= mature_TGF_beta_1
FT repeat_region 2015..2100
FT /tag= e
FT /note= "GC-rich region; possibly responsible for the
FT fact 3'UTR of mRNA could not be cloned as cDNA;
FT may be important for transcription efficiency"
FT repeat_unit 2019..2023
FT /tag= f
FT TATA_signal 2094..2100
FT /tag= g
FT /note= "TATA-like sequence; no evidence that this
FT functions a promoter"
FT polyA_signal 2514..2520
FT /tag= h
FT misc_signal 2529..2536
FT /tag= i
FT /note= "consensus sequence immediately precedes
FT polyA-tail (Benolst et al)"
XX
XX US5482851-A.
XX
XX 09-JAN-1996.
XX
XX 22-MAR-1985; 85US-0715142.
XX
XX 13-MAR-1987; 87US-0025423.
XX 22-MAR-1985; 85US-0715142.
XX 04-AUG-1989; 89US-0389929.
XX 04-MAR-1992; 92US-0845893.
XX 05-NOV-1993; 93US-0147364.
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XX XX
PA (GETH ) GENENTECH INC.
XX
PI Derynck RMA, Goeddel DV;
XX
DR WPI: 1996-076891/08.
DR P-PSDB: AAR90827.
XX
PT New recombinant human transforming growth factor-beta prods. - produced
PT using Chinese hamster ovary cells, for use in diagnostic applications
PT or in therapy
XX
PS Example 3; Fig 1; 26pp; English.
XX
CC The cDNA encodes the pre-transforming growth factor (TGF) beta 1 protein.
CC The nucleotide sequence was obt. by an analysis of several overlapping
CC cDNAs and gene fragments. The DNA is useful for the recombinant
CC production of TGF beta 1, which can be used in, e.g. wound healing.
CC (Revised entry submitted to correct sequence analysis breakdown.)
XX
SQ Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;

Query Match 71.9%; Score 978.8; DB 17; Length 2537;
Best Local Similarity 84.8%; Pred. No. 5e-188;
Matches 1146; Conservative 0; Mismatches 147; Indels 59; Gaps 2;

OY 6 CCGAGATGGCGCTTCGGGGCTCGCGCTCTTGGCCGCTGCTGCCGCTGTGGCTGC 65
DB 837 CCCCATGCGCGCCCTCGGGGCTGGCGCTGCTGCCCTGCTACCGCTGTGTGCTAC 896
OY 66 TAGTGTGACGCTGTGGCGGGCGCGCGCGGACCTGCCACCTGCAGAACATTCAGATG 125
DB 897 TGTGTGTGACGCTGTGGCGGGCGCGCGCGGACCTATCCAGCTGCAGATTCAGATG 956
OY 126 AGCTGTGAAGCGGAAGCGCATCGAGGCCATTCGGCGCCAGATTCTTCCAGCTTGGC 185
DB 957 AGCTGTGAAGCGGAAGCGCATCGAGGCCATTCGGCGCCAGATTCTTCCAGCTTGGC 1016
OY 186 TTGGCAGCCCCCGAGGCGAGGGGGAGCGCGCGCGCGCGCTGAGGAGTACTGG 245
DB 1017 TCGCGACCCCCCGAGGCGAGGGGGAGTGGCCGCCGCCGCTGCGCGCGCTGCTCG 1076
OY 246 CTCTTACACAGTACCCCGGAGCGGAGTACCGGGAGGATGTCGACCGGACCGGAGC 305
DB 1077 CCTGTACACAGCAGCCGCGAGCGGGTGGCGGAGGATGTCACACCGGACCGGAGC 1136
OY 306 CAGAGGGGAGCTACTAGCCAGAGAGTACCCGCGTCTAATGTGTGAACCGGACCC 365
DB 1137 CTGAGGCGGACTACTAGCCAGAGAGTACCCGCGTCTAATGTGTGAACCCACACAG 1196
OY 366 AATCTATGATTAATTCAGAGGCGACCCCGACAGCTTATATGCTGTTCACACAGTGG 425
DB 1197 AATCTATGATTAATTCAGAGGAGTACACACAGCATATATGTCTTCAACACATCAG 1256
OY 426 AGCTCCGGGAGGCGGTCGGAGACCTGTATGTCTCTCGGGCAGAGCTGCGCTGCTGA 485
DB 1257 AGCTCCGAGAGGCGGTACTGAAACCCGTGTCTCTCCGGGACAGCTGCGTGTGCTGA 1316
OY 486 GGCCTCAAGTTAAAGTGGAGCAGCAGCGAGCTATACCAAAATACAGCAATGATCT 545
DB 1317 GGCCTCAAGTTAAAGTGGAGCAGCAGCTGGAGCTGTACCAAAATACAGCAATTTCT 1376
OY 546 GGGGCTACCTCAGCAACCGGCTGTGCGCCCGCACTGACTACCGGAGGCGCTGCTTTG 605
DB 1377 GGGGATACCTCAGCAACCGGCTGTGCGCACCCACAGCTGCCAGAGTGTATTCTTTTG 1436
OY 606 ATGTACCGGAGTTGTGCGCAGTGTGACCCGCAAGAGGCTATAGAGGATTTTCGC 665
DB 1437 ATGTACCGGAGTTGTGCGCAGTGTGAGCCGTGGAAGGAAATTAAGGCTTTTCGC 1496
OY 666 TCAGTCCCACTCTTCCTCTGACAGCAAGATTAACACACTTCAGTGAATTAAGCGGT 725
DB 1497 TTAGCGCCCACTGCTCTGTGACAGCAGGATTAACACACTGCAAGTGCATCAACGGGT 1556
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QY	546	GGGGACACACACACACCGGCTGCTGGCCCGCCCACTAGCTACACGGAGTGGCTGCTCTTG	605
Db	1377	GGGGATACCTCACACACCGGCTCTGGCACCCACGACGCTGCCAGAGTGGTATCTTTTG	1438
QY	606	ATGTACCGGAGTTGTGTGCGCAGTGGCTGTGACCCGACAGAGAGGCTATAGAGGTTTGGCC	665
Db	1437	ATGTACCGGAGTTGTGTGCGCAGTGGCTGTGACCCGACAGAGAGGCTATAGAGGTTTGGCC	1496
QY	666	TCAGTGGCCACTTTCTCTGTGACAGCAAGATTAACACTTCACAGCTGAGGAAATTAACGGGT	725
Db	1497	TTAGCGCCCACTCTCTCTGTGACAGCAGGAGATTAACACTTCAGTGAATGACATCAACGGGT	1556
QY	726	TCAAATCTGGCCCGGGGAGACTGGCCCAACATTCACGGGATTAACCGCCCTTCTGCG	785
Db	1557	TCAGTACCGGGCCCGCAGGTGAGCTGTGCAACATTCATGTGATGAACCGGCTTCTGCG	1616
QY	786	TCCTCATGGCCACCCGCTGTGAGAGGGCCAGCACTGCACAGCTCCCGGACCGCCGAG	845
Db	1617	TTCTCATGGCCACCCGCTGTGAGAGGGCCAGCATGCTGCAAGAGTCCCGGACCGCCGA	1675
QY	846	CCCTGGATACAAACACTACCCATAGAGCTGGCAGACTGCAGATCTCTGTGGCCCTGATATA	905
Db	1676	-----GCCCTGTGACA	1685
QY	906	CCAACACTGCTTACAGCTCCACGAGAAAGAACTGCTGCGGACAGCTTACATTGACT	965
Db	1686	CCAACATTTGCTTACAGCTCCACGAGAAAGAACTGCTGCGGACAGCTTACATTGACT	1745
QY	966	TCCGGAGAGACCTGGGCTGTGAGTGAATTCATGAAACCCAAAGGGCTTACATGCCAATTTCT	1025
Db	1746	TTCCGGAAGAGACCTGGGCTGTGAGTGAATTCATGAAACCCAAAGGGCTTACATGCCAATTTCT	1805
QY	1026	GCCCTGGGGGCTGTGCCCTACATCTGAGGCTTAACACTGATGATACAGAGTCTGTGCTC	1085
Db	1806	GCCCTGGGGGCTGTGCCCTACATTTTGAAGCTGTGACACGCACTGACAGAAAGTCTTGCGCC	1865
QY	1086	TGTACAAACGACAAACCCGGGCGGCTGCGCGGCGGCTGCTGCTGCTGCGCCAGAGCGGTGG	1145
Db	1866	TGTACAAACGACATTAACCCGGGCGGCTGCGCGGCGGCTGCTGCTGCTGCGCCAGAGCGGTGG	1925
QY	1146	AGCCACTGCGCCATCTGTGTACTACGTGTGGGCGGCAAGCCCAAGGTGAGAGCACTGTCCACA	1205
Db	1926	AGCCGCTGCCCATCTGTGTACTACGTGTGGGCGGCAAGCCCAAGGTGAGAGCACTGTCCACA	1985
QY	1206	TGATGTGCTGTTCTCTGTCAAGTGCAGTGTGAGGCGCGCCCGCCCAAGCGCCGCCACCC	1265
Db	1986	TGATGTGCTGCTCTCTGTCAAGTGCAGTGTGAGTTCGCGCCCGCCCGCCCGCCGCCGAG	2045
QY	1266	GGCAGGCGCGGCGCCACCCCGCGCGCT-----CACGGGCTGTATTTAAGGACA	1317
Db	2046	GCCCGGCGCCACCCCGCGCGCGCGCTTGCCCATGTGGGGCTGTATTTAAGGACA	2105
QY	1318	TCGTGCCCCCAAGCCACTTGGGATGGATTAA	1349
Db	2106	CCGTGCCCAAGCCACTGTGGGGCGCCCATTA	2137

Result	7
AAV52933	
ID	AAV52933 standard; cDNA; 2537 BP.
XX	
AC	AAV52933;
XX	
DT	21-DEC-1998 (first entry)
XX	
DE	Human pre-transforming growth factor-beta 1 cDNA.
XX	
KM	Transforming growth factor-beta 1; TGF-beta 1; human; ss.
XX	
OS	Homo sapiens.
XX	
PH	key
	Location/Qualifiers

FT	CDS	842..2014
FT	/tag= a	
FT	mat_peptide	1676..2011
FT	/tag= b	
FT	stem_loop	37..113
FT	/tag= b	
FT	/note= "Putative stable hairpin loop"	
FT	misc_feature	2015..2100
FT	/tag= c	
FT	/note= "GC-rich sequence"	
FT	polyA_signal	2514..2520
XX		/tag= d
XX		
PN	US5801231-A.	
XX		
PD	01-SEP-1998.	
XX		
PF	22-MAR-1985;	85U5-0715142.
XX		
PR	13-MAR-1987;	87U5-0025423.
PR	22-MAR-1985;	85U5-0715142.
PR	04-AUG-1989;	89U5-0389929.
PR	04-MAR-1992;	92U5-0845893.
PR	05-NOV-1993;	93U5-0147364.
PR	30-MAY-1995;	95U5-0454468.
PA	(GETH) GENENTECH INC.	
XX		
PI	Derynck RMA, Goeddel DV,	
XX		
DR	WPI: 1998-494840/42.	
P	P-PSDB; AAW78785.	
PT	DNA encoding transforming growth factor-beta precursor sequence -	
PT	useful for analysis to perform manipulations to increase yield of	
PT	recombinant production of the protein	
XX		
PS	Example 3; Fig IB 1-3; 26pp; English.	
XX		
CC	This nucleotide sequence codes for the human transforming growth	
CC	factor-beta 1 precursor (preTGF-beta 1, see AAW78785). It is a	
CC	composite of overlapping cDNA clones isolated from different cDNA	
CC	libraries (placenta, A172 glioblastoma, HT1080 fibroblastoma) using	
CC	TGF-beta exon (see AAV52936) restriction fragments as probes.	
CC	The 3' region of the sequence was determined using cloned genomic	
CC	DNA. The invention relates to the recombinant production of	
CC	TGF-beta. Biologically active TGF-beta is defined as being capable	
CC	of inducing EGF-potentiated anchorage independent growth of target	
CC	cell lines and/or growth inhibition of neoplastic cell lines.	
CC	Nucleic acids encoding TGF-beta have been isolated and cloned into	
CC	vectors which are replicated in bacteria and expressed in	
CC	eukaryotic cells. TGF-beta recovered from transformed cells is	
CC	used in known therapeutic applications. TGF-beta nucleic acids are	
CC	also useful in diagnosis and identification of TGF-beta clones.	
XX		
SO	Sequence 2537 BP; 475 A; 895 C; 736 G; 431 T; 0 other;	
Query Match	71.6%; Score 974; DB 19; Length 2537;	
Best Local Similarity	84.5%; Pred. NO. 4,6e-187;	
Matches 1143; Conservative	0; Mismatches 150; Indels 59; Gaps	
OY	6 CCGAGATGCGCGCTTCGGGGGTGCGGCTCTTGCCGCTGCTGCCGCTGTGGCTGC	65
Db		
B37	CCCCATCCCGCCCGCCCGCGGCGTGGCTGCTACCGCTGCTACCGCTGTGGCTAC	896
OY	TAGTGTCAAGCGCTGGCGGCGCGCGCGCGGACTGTCCACCTGCAAGACCATCAGCATGG	125
Db		
B97	TGCTGTACCGCTTGCGCGCGCGCGCGGACTATTCACCTGCAAGACTATCAGCATGG	956
OY	AGCTGTGAAGCGCAAGGCATTCAGAGCCATTTCGGGCGAGATTGTGTCACAAGCTTCCGC	185
Db		
Bb	AGCAGGTAAACGCGAAGCGCATTCGAGGCGCATTCGCGGCGAGAATCTGTTCGAAGCTGCGCG	1016


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OY 186 TTGCGACCCCGGAGCGAGGAGCTGCCGCCGCCGCTGCTGAGGAGTACTGG 245
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 437 TCGCGACGCCCCCGAGCGAGGGGAGTGCGCCGCCGCCGCTGCCGAGGCCGTGCTG 436
OY 246 CTCTTTACACAGTACCCGCGAGCGGGTACCGGGGAAAAGTGTCCAGCCGAGCCGAGC 305
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 497 CCGTGTACACAGACCGCGACCGGGGTGGCGGGAGTGCAGGAGCCGAGCCCGAAC 556
OY 306 CAGAGCGGAGTACTAGAGCCCAAGAGAGTACCCCGGTGTAATGGTGAAGGGGCAACC 365
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 557 CGGAGCGGAGTACTAGAGCCCAAGAGAGTACCCCGGTGTAATGGTGAAGCCACACAG 616
OY 366 AAATCTATGATTAATTAAGGGCAACCCCGACAGCTTATATATGCTTCAACAGCTGG 425
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 617 AAATCTATGATTAAGTACAGAGACACACAGCATATATATGCTTCAACACATCAG 676
OY 426 AGCTCGGGGAAGGCGTGGCAACCTGATATGCTCTCTCGGCAAGCTCGGCTCTGA 485
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 677 AGCTCGAGAAAGCATGTAACCTGTGTGCTCTCCCGGCAAGCTGCGTCTCTGA 736
OY 486 GGCCTCAAGTTAAAGTGGAGCAGCAGTGAATACAGAAATACAGCAATGATTCCT 545
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 737 GGCCTCAAGTTAAAGTGGAGCAGTGAATGAGTGTACAGAAATACAGCAATTCCT 796
OY 546 GCGGCTACCTCAGACACCGGCTGCTGGCCCCAGTGACTCAACCGAGTGGCTGCTTTG 605
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 797 GCGGCTACCTCAGACACCGGCTGCTGGGCCACAGCATCGCCGAGTGTGCTTTG 856
OY 606 ATGTACCGGAGTGTGTCGGGAGTGGCTGACCCGAGAGAGGCTATAGAGGTTTTCGCC 665
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 857 ATGTACCGGAGTGTGTCGGGAGTGGCTGACCCGAGAGGAAATGAGGCTTTTCGCC 916
OY 666 TCAGTCCCACTCTCTCTGACAGCAAAAGATTAACACACTCCAGCTGGAATTAACGGGT 725
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 917 TTAGCCGCCACTCTCTCTGTGACAGCAAAAGATTAACACTGGAATGAGATCAACAGGCT 976
OY 726 TCAATCTGCGGCGCGGGGAGTGAATGACATTCACAGGATGAACCGGCTTCCTGC 785
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Db 977 TCAATCTGCGGCGCGGGGAGTGAATGACATTCAGGATGAACCGGCTTCCTGC 1036
OY 786 TCCCTATGCGCACCGGCTGGAGAGGCGCCAGCAGCTGACAGTCCCGGAGCCGCGAG 845
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Db 1037 TTCTATGGGCGACCCCACTGGAAGAGGCGCCCAACATCTGCAAAAGCTCCCGGACCCGCGA- 1095
OY 846 CCTGTGATACCAACAGCTACCAATAGCAGTGCAGACTGCTGTGCGCTGGATTA 905
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Db 1096 -----GCCCTGGACA 1105
OY 906 CCAACTACTGCTTCCAGCTCCAGGAGAAAGACTGTGCGTGGAGCTTATACATGACT 965
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1106 CCAACTACTGCTTCCAGCTCCAGGAGAAAGACTGTGCGTGGAGCTTATATGACT 1165
OY 966 TCCGGAAGAGTCTGGGCTGGAATGATATGAAACCAAGGGTATACATGCCAATTTCT 1025
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1166 TCCGGAAGAGTCTGGGCTGGAATGATATGAAACCAAGGGTATACATGCCAATTTCT 1225
OY 1026 GCGTGGGCGCTGCTCCCTCATCTGAGAGCTTGAACACTCACTAAGCAAGTCTTGCTC 1085
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Db 1226 GCGTGGGCGCTGCTCCCTCATCTGAGAGCTTGAACACTCACTAAGCAAGTCTTGCTC 1285
OY 1086 TGTACAAACAGCAACACCGGCGGCTGCGGCGCGCTGCTGCGAGGAGGCTGG 1145
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Db 1286 TGTACAAACAGCAACACCGGCGGCTGCGGCGCGCTGCTGCGAGGAGGCTGG 1345
OY 1146 AGCCACTGCGCAATGCTGTAATAGTGGGCGCAAGCCCAAGGTGAGAGTGTCCACA 1205
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OY 1266 GCGAGGCCCGGCCACCCCGCGCT-----CACCGGGCTGTATTTAAGACA 1317
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RESULT 9
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ID AAT58342 standard; cDNA; 2742 BP.
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AC AAT58342;
XX
DT 22-OCT-2001 (first entry)
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DE Human polynucleotide SEQ ID NO 545.
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KW Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; SS.
XX
OS Homo sapiens.
XX
PN NO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000MO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 03-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSE0 INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
XX
XX P-PSDB; AAM39186.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX PT such as central nervous system injuries -
XX PS Claim 1; SEQ ID NO 545; 1007bp; English.
XX
XX The invention relates to human nucleic acids (AAT57798-AAT61369) and
XX CC the encoded polypeptides (AAM38642-AAM4213) with neotropic,
XX CC immunosuppressant and cytostatic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localised neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilisation of the activities such as: Immune system suppression,
XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemias and
XX CC C.N.S disorders.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification.
```


PT preparing DNA chain contig. base sequence coding for human
 PT prepro-TGF-beta 1, forming expression vector etc.

PS Claim 1; Fig 1; 16pp; Japanese.

CC The DNA sequence encodes human prepro-TGF-beta 1 which can be
 CC produced by recombinant methods, it has osteogenic and
 CC tumoricidal activity.

XX Sequence 1821 BP; 326 A; 679 C; 508 G; 308 T; 0 other;

Query Match 71.1%; Score 968.2; DB 12; Length 1821;
 Best Local Similarity 84.9%; Pred. No. 6,5e-186;
 Matches 1133; Conservative 0; Mismatches 143; Indels 59; Gaps 2;

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 507 CCCCCATGGCGCCTCGGGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 566
 66 TAGTGTGACGCTGGCGGGCGCGCGCGGACTGTCACCTGCAAGACATGCATGATG 125
 11
 567 TGGTGTGACGCTGGCGGGCGCGCGGACTGTCACCTGCAAGACATGCATGATG 626
 126 AGCTGTGAAGCGGAAGCGCATGAGGCGCATTCGCGCGAGATTCTGTCAGCTTGGC 185
 627 AGCTGTGAAGCGGAAGCGCATGAGGCGCATTCGCGCGAGATTCTGTCAGCTTGGC 686
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 687 TGGCGAGCCCCCGGAGCGAGAGAGTGGCGCGCGCGCGCTGCTGTCAGAGTGG 746
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RESULT 12

AA81084
 ID AA81084 standard; cDNA; 1560 BP.

AA81084;

09-OCT-1990 (first entry)

Coding sequence of simian transforming growth factor-beta 1.

Transforming growth factor-beta 1; tumour treatment; ss cDNA.

Cercopithecus aethiops.

Key Location/Qualifiers

CDS 261..1433

FT /tag= a

FT sig_peptide 282..323

FT mat_peptide 1095..1433

FT /tag= c

EP293785-A.

07-DEC-1988.

27-MAY-1988; 88EP-0108528.

29-MAY-1987; 87US-0055662.

25-JAN-1988; 88US-0147842.

(ONCO-) ONCOGEN.

Purchio AF, Gentry L, Twardzik D;

WPI; 1988-347488/49.

F-PDB; AP80647.

GenCore version 5.1.4_p5_4578
(c) 1993 - 2003 CompuGen Ltd.

using sw model

03, 10:33:16 ; Search time 70 Seconds
(without alignments)

5962.672 Million cell updates/sec

2E-36

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Gapext 1.0

153338381 residues

ing chosen parameters: 882724

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ch 08

st 45 summaries

nts_NA: *

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ptodata1/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Category	Match Length	DB	ID	Description
13.7	2537	6	5168051-1	Patent No. 516805-1
13.4	1560	1	US-07-669-171-1	Sequence 1, App
13.3	2745	4	US-09-661-753-28	Sequence 28, App
13.3	2745	5	PCT-US94-03705-3	Sequence 3, App
13.4	1569	1	US-07-669-171-3	Sequence 3, App
13.4	2094	4	US-09-661-753-1	Sequence 1, App
13.4	1585	4	US-09-661-753-1	Sequence 27, App
13.4	2207	6	5221620-3	Patent No. 52216
13.4	339	1	US-08-470-837-29	Sequence 29, App
13.4	339	1	US-08-486-0578-1	Sequence 1, App
13.4	339	2	US-08-789-588-1	Sequence 1, App
13.4	339	3	US-09-123-233-1	Sequence 1, App
13.4	337	4	US-08-868-452-29	Sequence 29, App
13.4	2671	6	5168051-9	Patent No. 516805
13.4	2529	5	PCT-US91-004541-1	Sequence 1, App
13.4	2529	6	5262319-1	Patent No. 52623
13.4	2574	4	US-09-380-662-20	Sequence 20, App
13.4	336	3	US-09-123-233-7	Sequence 7, App
13.4	339	1	US-08-486-0578-3	Sequence 3, App
13.4	339	1	US-08-470-837-33	Sequence 33, App
13.4	339	2	US-08-789-588-3	Sequence 3, App
13.4	339	3	US-09-123-233-5	Sequence 5, App
13.4	339	4	US-09-000-069A-1	Sequence 1, App
13.4	2173	6	5168051-10	Patent No. 516805
13.4	336	3	US-09-123-233-11	Sequence 11, App
13.4	336	3	US-09-123-233-9	Sequence 9, App

28	179.8	13.2	4.667	4	US-09-661-753-47	Sequence 47, Appl
29	158.2	11.6	339	1	US-08-486-057B-2	Sequence 2, Appl1
30	158.2	11.6	339	1	US-08-470-837-31	Sequence 31, Appl
31	158.2	11.6	339	2	US-08-789-588-2	Sequence 2, Appl1
32	158.2	11.6	339	3	US-09-123-233-3	Sequence 3, Appl1
33	158.2	11.6	1695	5	PCR-US64-03705-4	Sequence 4, Appl1
34	153	11.6	2669	6	522162620-1	Patent No. 522162620
35	140	10.3	575	6	5168053	Patent No. 5168053
36	130.4	9.6	339	4	US-08-668-452-31	Sequence 31, Appl
37	68.8	5.1	110	1	US-07-668-648-11	Sequence 11, Appl
38	68.8	5.1	110	2	US-08-429-998-11	Sequence 11, Appl
39	68.8	5.1	110	2	US-08-431-333-11	Sequence 11, Appl
40	68.8	5.1	110	5	PCR-US91-02323-11	Sequence 11, Appl
41	62.6	4.6	5578	1	US-08-081-610-2	Sequence 2, Appl1
42	50.4	3.7	658	2	US-08-621-803-254	Sequence 254, Appl
43	50.4	3.7	658	4	US-09-217-352-254	Sequence 254, Appl
44	50.4	3.7	894	1	US-07-764-731B-3	Sequence 3, Appl1
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ALIGNMENTS

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RESULT 2

US-07-669-171-1
Sequence 1, Application US/07669171

Patent No. 5304541
GENERAL INFORMATION:

APPLICANT: PURCHIO, ANTHONY F.
APPLICANT: MADISEN, LINDA

APPLICANT: MERRIN, JUNE RAE
TITLE OF INVENTION: TGF- β 1/D2: A NOVEL CHIMERIC TRANSFORMING

TITLE OF INVENTION: TGF- β 1/D2: A NOVEL CHIMERIC TRANSFORMING
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS

```

? STREET: 1155 AVENUE OF THE AMERICAS
? CITY: NEW YORK
? STATE: N.Y.
? COUNTRY: U.S.A.
? ZIP: 10036
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/669,171
? FILING DATE: 19910314
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: MISROCK, S. LESLIE
? REGISTRATION NUMBER: 18,872
? REFERENCE/DOCKET NUMBER: 5624-159-999
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212-790-9090
? TELEFAX: 212-869-9741
? TELEX: 66141 PENNIE
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1560 base pairs
? TYPE: NUCLEIC ACID
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 261..1430
? US-07-669-171-1

Query Match 71.3%; Score 970.8; DB 1; Length 1560;
Best Local Similarity 85.0%; Pred. No. 8e-197;
Matches 1146; Conservative 0; Mismatches 142; Indels 60; Gaps 3;

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US-09-661-753-28			
Sequence 28, Application US/09661753			
Patent No. 6436909			
GENERAL INFORMATION:			
APPLICANT: Nicholas M. Dean			
APPLICANT: Susan F. Murray			
TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA			
FILE REFERENCE: ISPh-0498			
CURRENT APPLICATION NUMBER: US/09/661,753			
CURRENT FILING DATE: 2000-09-14			
EARLIER APPLICATION NUMBER: 60/154,546			
EARLIER FILING DATE: 1999-09-17			
NUMBER OF SEQ ID NOS: 68			
SEQ ID NO 28			

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Db 1806 TCTGCTGGGGGCTGTCTCTACATCTGAGGCTGAGACCTGACACTGATACAGCAAGGCTGTG 1865
QY 1083 CTCTGTACAAACGACCAACCCGGGGGCTGTGGGGGCTGTGGTGTGCTGCTGCGAGGCGC 1142
Db 1866 CCTGTACAAACGACCAACCCGGGGGCTGTGGGGGCTGTGGTGTGCTGCTGCGAGGCGC 1925
QY 1143 TGGAGCCACTGCCCATCTGTGTACTAGCTGAGGCGCAAGCCCAAGAGTGGAGAGCTGTCCA 1202
Db 1926 TGGAGCCACTGCCCATCTGTGTACTAGCTGAGGCGCAAGCCCAAGAGTGGAGAGCTGTCCA 1985
QY 1203 ACATGATGCTGCTTCTCTGCAATGCAAGCTGAGGCGCCCGCCCGCCCAAGCCCGCCCA 1262
Db 1986 ACATGATGCTGCTTCTCTGCAATGCAAGCTGAGGCGCCCGCCCGCCCGCCCGCCCGC 2045
QY 1263 CCGGAGGCGCCGCGCCCAACCCCGCCCGCT-----CACCGGGGCTGTATTAAAG 1314
Db 2046 CAGGCGCGCGCCCAACCCCGCCCGCT-----CACCGGGGCTGTATTAAAG 2105
QY 1315 ACATGCTGCCCAAGCCCACTGGGATGATTAATA 1349
Db 2106 ACACGCTGCCCAAGCCCACTGGGAGTCCCATTA 2140

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RESULT 4

PCT-US94-03705-3

Sequence 3, Application PC/TUS9403705

GENERAL INFORMATION:

APPLICANT: Mark A. Perrella

TITLE OF INVENTION: TRANSFORMING GROWTH

TITLE OF INVENTION: FACTOR- INHIBITS

TITLE OF INVENTION: INDUCIBLE NITRIC OXIDE

TITLE OF INVENTION: SYNTHASE GENE

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/03705

FILING DATE: 5 April 1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Janis K. Fraser

REGISTRATION NUMBER: Reg. No. 34, 819

REFERENCE/DOCKET NUMBER: 05433/007001

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ. ID NO: 3:

SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 2745
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US94-03705-3

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Query Match 71.0%; Score 965.8; DB 5; Length 2745;
Best Local Similarity 84.6%; Pred. No. 9, 9e-196;
Matches 1146; Conservative 0; Mismatches 147; Indels 62; Gaps 3;

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QY 6 CGAGATGCGGCTTGGGGGCTGCGGCTGTGGCGTGGCGGCTGCTGTGGCTGCTGTGGCTG 65
Db 837 CCGCATGCGGCTTGGGGGCTGCGGCTGTGGCGTGGCGGCTGCTGTGGCTGCTGTGGCTG 896
QY 66 TAGTGTGACGCTTGGCGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 125
Db 897 TGGTGTGACGCTTGGCGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 956
QY 126 AGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 185
Db 957 AGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1016
QY 186 TTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 245
Db 1017 TTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1076
QY 246 CTCTTACAGAGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 305
Db 1077 CCGTGTACAGAGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1136
QY 306 CAGAGCGCGAGTACTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 365
Db 1137 CTGAGCGCGAGTACTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1196
QY 366 AATCTATGATTAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 425
Db 1197 AATCTATGATTAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1256
QY 426 AGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 483
Db 1257 AGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1316
QY 484 -GAGCTCAAGTAAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 542
Db 1317 GAGGCTCAAGTAAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1376
QY 543 CTGCGGCTACCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 602
Db 1377 CTGCGGCTACCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1436
QY 603 TTGATGTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 662
Db 1437 TTGATGTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1496
QY 663 GCTCAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 722
Db 1497 GCTCAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1556
QY 723 GATTCAATTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 782
Db 1557 GATTCAATTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1616
QY 783 TGTCTCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 842
Db 1617 TGTCTCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1676
QY 843 GAGCGCTGATACCAACAGGTAACCAATACAGCTGCCAGACTACGATCTGTGCGCGCTGG 902
Db 1677 GA-----GCCCTGG 1685
QY 903 ATACCACTACTGCTTACAGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 962
Db 1686 ACACCACTATTTGCTTACAGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1745

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1028 CTGGGCGCTGCTCCCTACATCTGAGAGCTAGACACTAGTACAGCAGAGTCTGCTCTG 1087
1236 CTGGGCGCTGCTCCCTACATCTGAGAGCTAGACACTAGTACAGCAGAGTCTGCTCTG 1295
1088 TTCAACACAGACACACCGGGGCGCTCGGGGCGCTGCTGCTGCTGCTGCTGCTGCTG 1147
1296 TACAAACACACATTAACCGGGGCGCTCGGGGCGCTGCTGCTGCTGCTGCTGCTGCTG 1355
1148 CCAGTCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1207
1356 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1415
1208 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1267
1416 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1475
1268 CAGGCG 1318
1476 CCGGCG 1535
1319 CGTGGCCCAAGCCCACTGGGAGTGAATTA 1349
1536 CGTGGCCCAAGCCCACTGGGAGTGAATTA 1566

RESULT 6
US-09-661-753-1

; Sequence 1, Application us/09661753

; Patent No. 6436909

; GENERAL INFORMATION:

; APPLICANT: Nicholas M. Dean

; APPLICANT: Susan F. Murray

; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA

; FILE REFERENCE: ISPH-0498

; CURRENT APPLICATION NUMBER: US/09/661,753

; EARLIER FILING DATE: 2000-09-14

; EARLIER APPLICATION NUMBER: 60/154,546

; NUMBER OF SEQ ID NOS: 68

; SEQ ID NO 1

; LENGTH: 2094

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (868)..(2040)

US-09-661-753-1

Query Match 62.2%; Score 847; DB 4; Length 2094;

Best Local Similarity 80.8%; Pred. No. 1.2e-170; Mismatches 190; Indels 57; Gaps 2;

Matches 1038; Conservative 0; Mismatches 190; Indels 57; Gaps 2;

6 CCGAGATGGGCGCTTGGGGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 65
863 CCGGCGCGCGCGCTTGGGGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 922
66 TAGTGTGAGCGCTTGGGCG 125
923 TAGTGTGAGCG 982
126 AGCTGTGAGCG 185
983 AGCTGTGAGCG 1042
186 TTGCGGCG 245
1043 TCGGCG 1102
246 CTCTTTAACAACAGTACCG 305
1103 CTCTTTAACAACAGTACCG 1162
306 CAGAGCG 365

1163 CCGAGGCGGAGTACTATCTTAAAGAGGTACACCGCGCTGCTAATGGGAGACCGCAACG 1222
366 AATCTTATGATTAATTCAGAGGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 425
1223 CCATCTATGAGAAACCAAGACATCTACACAGATATATATATATATATATATATATAT 1282
426 AGCTCCGGGAGCGGTGGCGGAACTGATTTGCTCTCTGCGGCGAGAGTGGCTGCTGA 485
1283 ACATTCGGGAGAGTGGCGGCGGAACTGATTTGCTCTCTGCGGCGAGAGTGGCTGCTGA 1342
486 GGTTCAGTTAAAGTGGAGAGCACTGAGAGTATACAGAAATACAGAAATACAGAAATAC 545
1343 GATTAATTAAGTGGAGAGCACTGAGAGTATACAGAAATACAGAAATACAGAAATAC 1402
546 GGGCGTACCTGAGCAACCG 605
1403 GGGCGTACCTGAGTACCG 1462
606 ATGTACCGGAGTGTGGCGCGAGTGTGACCGCGCGAGAGGCTATAGAGGCTTTTCGCC 665
1463 AGTTCAGTGGAGTGTGGCGCGAGTGTGACCGCGCGAGAGGCTATAGAGGCTTTTCGCAT 1522
666 TCAATTCG 725
1523 TCAGCGCTACCTGCTCTGTGACAGCAAGATTAACACACTCCAGTGAATTAAGCGGT 1582
726 TCAATTCG 785
1583 TCAGCGCTACCTGCTCTGTGACAGCAAGATTAACACACTCCAGTGAATTAAGCGGT 1642
786 TCGTCATGCG 845
1643 TCGTCATGCG 1701
846 CCGTGGATACCAACAGTACCATACAGAGTGGCGAGATACAGATCTGCGCGCGTGA 905
1702 -----GCCGTGATA 1711
906 CCAACTACGCTTTCAGCTCCACGAGAGAAAGTGTGCTGCGCGCGCGCGCGCGCGCGCG 965
1712 CCAACTACGCTTTCAGCTCCACGAGAGAAAGTGTGCTGCGCGCGCGCGCGCGCGCGCG 1771
966 TCCGAGAGGAGCTGGGCTGGAAGTGTATCAAGACCCCAAGGCTTACATGCTTCTTCT 1025
1772 TTAGGAAAGAGCTGGGCTGGAAGTGTATCAAGACCCCAAGGCTTACATGCTTCTTCT 1831
1026 GCGTGGGCG 1085
1832 GTCTGGGAGCTGCG 1891
1086 TGTACAAACAGCAACCG 1145
1892 TGTACAAACAGCAACCG 1951
1146 AGCACTGCG 1205
1952 AGCACTGCG 2011
1206 TGTATGCG 1265
2012 TGTATGCG 2065
1266 GCGAGGCG 1290
2066 GCGAGGCG 2090

RESULT 7
US-09-661-753-27
; Sequence 27, Application us/09661753
; Patent No. 6436909
; GENERAL INFORMATION:

OY	186	TTGCGAGCCCCCGAGAGCCAGGGGAGAGTGTCGCGCCGAGCCCGCTGCTCGAGAGCACTACG	245
Db	436	TCGCCAGCCCCCGAGAGCCAGGGGAGAGTGTCGCGCCGAGCCCGCTGCTCGAGAGCACTACG	495
OY	246	CTCTTACACAGTACCCGCGAGACCGGGTAGCCGGGGAGAGTGTGAAACGGAGCCGAGC	305
Db	496	CCCTGTACACAGCAGCACCCTCGAGCCGGGTGGCCGGGAGAGACGGCGGAGCCGAGCCCGAC	555
OY	306	CAGAGGGGAGACTACAGCCGAGAGAGGTACCCCGCGTCAATAGTGTGAAAGGGGCAACC	365
Db	556	CGAGGCCGAGCTACTACAGCCAGAGAGAGTACCCCGCGTCAATAGTGTGAAAGGGGCAACC	615
OY	366	AAATCTATGATAAATTCAGAGGGCACCCTCCAGACTTATATGCTGTTCAACACGTCGG	425
Db	616	AAATCTATGATAAATTCAGAGGGCACCCTCCAGACTTATATGCTGTTCAACACATCAG	675
OY	426	AGCTCCGGGAGAGCGGTGCCGGAACCTGTATGTCTCTCGGGCAGAGACTGCGCTGCTGA	485
Db	676	AGCTCCGGGAGAGCGGTGCCGGAACCTGTATGTCTCTCGGGCAGAGACTGCGTGTGCTGA	735
OY	486	GACCTCAAGTTAAAGTGTGAGCAGACAGTGGAGCTTATACAGAAATACAGAAATGATTCCT	545
Db	736	GACCTCAAGTTAAAGTGTGAGCAGACAGTGGAGCTTATACAGAAATACAGCAACATTCCT	795
OY	546	GAGCGCTACCTCAGCAACCGGGCTGTGGCCCCCAGTACATCACCGAGTGGCTGTCTTTG	605
Db	796	GAGCGCTACCTCAGCAACCGGGCTGTGGCCCCCAGTACATCACCGAGTGGCTGTCTTTG	855
OY	606	ATGTACACGGAGGATTGTGGGGCAGTGGCTACCCGCGAGAGAGGCTATATGAGGGTTTGGCC	665
Db	856	ATGTACACGGAGGATTGTGGGGCAGTGGCTACCCGCGAGAGAGGCTATATGAGGGCTTGGCC	915
OY	666	TCAGTGCACCACTCTCTCTGTGACAGCAAGATATACACACTCCACGTTGGAATTAAACGGGT	725
Db	916	TTAGAGGCCACTGCTCTCTGTGACAGCAAGATATACACACTGCAAGTGGACATCAACGGGT	975
OY	726	TCATATTCGCGCGCGCGGGGTACCTTGGCCACCCTTACAGGCAATGAACCGGCGCTTCTGC	785
Db	976	TCACACTACGGCGCGCGAGGTGACCTGGCCACAATTCATGCAATGAACCGGCGCTTCTGC	1035
OY	786	TCCTCATGCGCACCCCGCGTGGAGAGGGCCAGACCTGACACACTCCCGGCGACCGCGAG	845
Db	1036	TTTCATGCGCACCCCGCGTGGAGAGGGCCACACATCTGCAAACTCCCGGCGACCGCGGA	1094
OY	846	CCCTGGATACCAACAGCTACCCCATACGAGCTGCCAGACTACGATCTGTGGCCCTGATATA	905
Db	1095	-----GCTTTGGATC 1104	
OY	906	CCAACCTACTGCTTCAGCTCCACGAGAAACGCTGCGTGGCGAGCCTGTACTATTGACT	965
Db	1105	CGGCTATTTGCTTTAGAAATGTGACAGCAATATTTGCTGCTACGCTCCACTTTACTTATTT	1164
OY	966	TCGCGAAGAGACCTGGGCTGGAAGTGGATTCAATGAACCAAGGGCTACCATGCCAATTTCT	1025
Db	1165	TCAGAGAGGAGTCTAGGGTGGAAATGATACAGAACCCAAAGGGTACAAATGGCAATTCCT	1224
OY	1026	GCGTGGGGCCCTGTGCCCTACACTCTGAGCGCTTAGACACTAGTACAGCAAGTCTGCGCTC	1085
Db	1225	GTGCTGGAGCAATGCCCGGATTTATTTAGATTCAGACACTAGCAGCACACAGGGTCTGGAGCT	1284
OY	1086	TGTACAAACAGACAAACCGGGCGGTGCGGCGCGCGCTGCTGCTGAGCCAGGCGGTGG	1145
Db	1285	TATATTAATACCAATAATCCAGAGCATCTGCTTCTTCTGTGCTGCTGTGCCAGATTTAG	1344
OY	1146	AGCCACTGCCCCTGCTGATCTAGTGTGGCCGAGAGCCAGAGGTGAGAGCACTGTCCACA	1205
Db	1345	AACCTCAACCATCTCTACTACATTTGGCAAAACACCAGAAATTTGAACAGCTTTCTATATA	1404
OY	1206	TGATGTGCGGTTTCTCGCAAGTCCAGCTGA 1234	
Db	1405	TGATGTGAGGCTTGTGCAAAATCCAGCTAA 1433	

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RESULT 9
US-08-470-837-29
; Sequence 29, Application US/08470837
; Patent No. 3600811
; GENERAL INFORMATION:
; APPLICANT: Nimm1, Marcel E.
; APPLICANT: Hall, Frederick L.
; APPLICANT: Tuan, Tai-Lan
; APPLICANT: Wu, Lingtao
; APPLICANT: Cheung, David T.
; TITLE OF INVENTION: Transforming Growth Factor B Fusion
; TITLE OF INVENTION: and
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,837
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Janice A.
; REGISTRATION NUMBER: 34,051
; REFERENCE/DOCKET NUMBER: 30630-1US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..333
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1
; US-08-470-837-29

Query Match          22.8%; Score 310.2; DB 1; Length 339;
Best Local Similarity 94.7%; Pred. No. 2, 9e-57;
Matches 321; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 896 GCCTGTGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCAGCGCAGCTC 955
    |||||
Db 1 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCAGCGCAGCTG 60

QY 956 TACATNTGACTTCCGGAGAGAGACTGGCGTGGAAGTGGATTTATGAAACCAAGGCTACCAT 1015
    |||||
Db 61 TACATNTGACTTCCGCAAGAGACTCGGCTGGGAAGTGGATTCATGAGGCCAAGGCTACCAT 120

QY 1016 GCCATTTCCTCGCTGGGGCCCTGTCCCTACATCTTGGAGCCTAGAACACTCACTAGACGAAG 1075
    |||||
Db 121 GCCAAGTTCTGCGCTCGGGCCCTGCCCCCTACATTTTGGAGCCCTGGAGACCGCACTATACAGCAAG 180

QY 1076 GTCTCGGCTGTATCAACAACAGCACACCAGCCGGGGCGCGTGGCGGCGCGTGGCTGCGTCCG 1135
    |||||

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Db 181 GTCTGCGCCCTGTACAAACGACATACCCGGCGCCCTGCGCGCCCTGCTGCGCTGCCG 240
QY 1136 CAGCGCGCTGGAGCCACTGCCCATCTGTACTACGTGGGCGCCGCAAGCCCAAGGTGGAGCAG 1195
|||||
Db 241 CAGCGCGCTGGAGCCGCGCTGCCCATCTGTACTACGTGGGCGCCGCAAGCCCAAGGTGGAGCAG 300
QY 1196 CTGTCCACATGATCTGTGGCTTCTCTGCAAGTGCAGCTGA 1234
|||||
Db 301 CTGTCCACATGATCTGTGGCTTCTCTGCAAGTGCAGCTGA 339

RESULT 10
US-08-486-057B-1
; Sequence 1, Application US/08486057B
; Patent No. 5650494
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,057B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: No. 5650494ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..339
FEATURE:
NAME/KEY: CDS
LOCATION: 1..339
US-08-486-057B-1

Query Match 22.7%; Score 308.6; DB 1; Length 339;
Best Local Similarity 94.4%; Pred. No. 6..4e-57;
Matches 320; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 896 GCCCTGATACCACTACTGCTTCACTCCAGGAGAAAGACTGCTGCGGCACTC 955
|||||
Db 1 GCCCTGAGACCACTATTGCTTCACTCCAGGAGAAAGACTGCTGCGGCACTC 60
QY 956 TACATGACTTCCGGAAGACCTGGGCTGGAAGTGAATCATGACCAAGGCTTACAT 1015
|||||
Db 61 TACATGACTTCCGGAAGACCTGGGCTGGAAGTGAATCATGACCAAGGCTTACAT 120
QY 1016 GCCAATTTGCTGGGAGCCCTGCTCCCTACATCTGAGACCTAGACACTGACAGCAAG 1075
|||||
Db 121 GCCAATTTGCTGGGAGCCCTGCTCCCTACATCTGAGACCTAGACACTGACAGCAAG 180
QY 1076 GTCTGCTGTCTGTACAAACGACAAACCCGGGCGCTGCGGCGCGCTGCTGCTGCCG 1135
|||||
Db 181 GTCTGCGCCCTGTACAAACGACAAACCCGGGCGCTGCGGCGCGCTGCTGCTGCCG 240

QY 1136 CAGCGCGCTGGAGCCACTGCCCATCTGTACTACGTGGGCGCCGCAAGCCCAAGGTGGAGCAG 1195
|||||
Db 241 CAGCGCGCTGGAGCCGCTGCCCATCTGTACTACGTGGGCGCCGCAAGCCCAAGGTGGAGCAG 300
QY 1196 CTGTCCACATGATCTGTGGCTTCTCTGCAAGTGCAGCTGA 1234
|||||
Db 301 CTGTCCACATGATCTGTGGCTTCTCTGCAAGTGCAGCTGA 339

RESULT 11
US-08-789-588-1
; Sequence 1, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,588
FILING DATE:
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989

QY	6	CCGAGATGGGCGCTTGGGGAGTGGCGCTCTTCACCGTGTGTGCTGGCGGTGCTGTGGTGC	65
Db	837	CCCCCATGCCCGCCCTCGGGGCTGGGCTCTCCCGCTGTGTCTACCGCTGCTGTGGTAC	896
QY	66	TATGGCGAGCGGCTGGCGCGCGCGCGCGGAGCTGCACCTGGCAAGACCATCGACATGG	125
Db	897	TGTGTCTGAGCGCTGGCGCGCGCGCGGAGCTATCCACTGCAAGACTATCGACATGG	956
QY	126	AGCTGTGTAAGCGGAAGCGCATGAGGCCATTGCGCGCCGAGATTCTGTCCAAAGCTTGGC	185
Db	957	AGCTGTGTAAGCGGAAGCGCATGAGGCCCATCGCGGCGCGAGTCTGTCCAAAGCTGCGGC	1016

186 TTGCGAGCCCCCGAGCGAGGAGCGTGCCTGCGCGCGCTGCTGAGCAGTACTGG 245
1017 TGGCCAGCCCCCGAGCGAGGAGGAGTGCCTGCGCGCGCTGCTGAGCAGTACTGG 1076
246 CTCCTTACACAGTACCGCGAGCGGGTACCGGGGAAAAGTGTGACCGCGAGCCGAGC 305
1077 CCTGTACAAACAGACCCCGGAGCGGGTGCCTGGGAGAGTGCAGAACCGGAGCCGAGC 1136
306 CAGAGCGGAGCTACTACGCGAGGAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 365
1137 CTGAGGCGCGCTACTACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1196
366 AATATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 425
1197 AATATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1256
426 AGCTCCGGGAGAGGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 483
1257 AGCTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1316
484 -GAGGCGCAAGTTAAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 542
1317 GAGGCGCAAGTTAAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1376
543 CCGGCGCTACTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 602
1377 CCGGCGCTACTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1436
603 TTGATGTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 662
1437 TTGATGTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1496
663 GCGTCAGTGCCTACT 722
1497 GCGTCAGTGCCTACT 1556
723 GGTTCATTTCTGGCGCGCGGGGAGTACCTGCGCCACCATTCACGCGCATGAACCGGCTTC 782
1557 GGTTCATTTCTGGCGCGCGGGGAGTACCTGCGCCACCATTCACGCGCATGAACCGGCTTC 1616
783 TGTCTCTCATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 842
1617 TGTCTCTCATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1676
843 GAGCCCTGATACCAAGCTACCATACGAGTGCAGACTACGATCTGCGCCCTGG 902
1677 GA-----GCGCTGG 1685
903 ATACCACTACTGCTTCACTGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 962
1686 ACACCACTACTGCTTCACTGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1745
963 ACTTCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1022
1746 ACTTCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1805
1023 TGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1082
1806 TGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1865
1083 CTCCTGTAACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1142
1866 CCTGTGTAACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1925
1143 TGGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1202
1926 TGGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1985
1203 ACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1262
1986 ACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2045
2045 CCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1314

Db 2046 CAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2105
QY 1315 ACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1349
Db 2106 ACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2140
RESULT 2
US-09-948-002-1
? Sequence 1, Application US/09948002
? Publication No. US20030050265A1
? GENERAL INFORMATION:
? APPLICANT: Nicholas M. Dean
? APPLICANT: Susan F. Murray
? TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
? FILE REFERENCE: ISPH-0607
? CURRENT APPLICATION NUMBER: US/09/948,002
? PRIOR FILING DATE: 2000-09-05
? PRIOR APPLICATION NUMBER: 09/661,753
? PRIOR FILING DATE: 2000-09-14
? PRIOR APPLICATION NUMBER: 60/154,546
? NUMBER OF SEQ ID NOS: 71
? SEQ ID NO 1
? LENGTH: 2094
? TYPE: DNA
? ORGANISM: Mus musculus
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (868)...(2040)
US-09-948-002-1
Query Match 62.2%; Score 847; DB 9; Length 2094;
Best Local Similarity 80.8%; Pred. No. 2,2e-219;
Matches 1038; Conservative 0; Mismatches 190; Indels 57; Gaps 2;
QY 6 CCGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 65
Db 863 CCGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 922
QY 66 TAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 125
Db 923 TAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 982
QY 126 AGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 185
Db 983 AGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1042
QY 186 TTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 245
Db 1043 TTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1102
QY 246 CTCCTTACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 305
Db 1103 CTCCTTACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1162
QY 306 CAGAG 365
Db 1163 CAGAG 1222
QY 366 AATATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 425
Db 1223 CCAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1282
QY 426 AGCTCCGGGAGAGGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 485
Db 1283 ACATTCGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1342
QY 486 GAGTCAAGTAAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 545
Db 1343 GATTAAATCAAGTGTGAGCAACATGTGAGACTTACAGAAATTAATTAATTAATTAATTA 1402

Qy	546	GGCGTACTCTGACGAACCGGCGTGGGCCCGCCAGTACTACACCGGAGTGGCTTCCTTG	605
Db	1403	GGCGTTACTCTTGGTAACCGGCGTGTACCCCACTGATACGGCTGTAGTGGCTCTCTTTG	1462
Qy	606	ATGTCACCGGAGTGTGGCGGAGTGGCTGACCAGACAGAGGCTATAGAGGCTTTCGCC	665
Db	1463	ACGTACCTGGAGTTGTACGGCAGTGGCTGAACCAAGGAGACGGGAATACAGGGCTTTCGAT	1522
Qy	666	TCAGTGGCCACTCTTCCTCTGTGACAGCAAAAGATTAACAACCTCCACGTGGAAATTAAGGGT	725
Db	1523	TCAGCGTCACTGCTCTTCTGTGTACACCAAAAGATTAACAACCTCCACGTGGAAATTAAGGGG	1582
Qy	726	TCAATTCGTGGCGCGGGGGGTGACCTGGCCACCATTTACGGCATGAACCGGCCCTTCCTGC	785
Db	1583	TCAGCGCCCAACAGTGGGGGCGACCTGGACCATTCATGATGAATGAACGGCCCTTCCTGC	1642
Qy	786	TCTCTCATGGCCACCCCGCTGTGAGAGGGCCACAGCACTGACAGCTCCCGCACCGCCGAG	845
Db	1643	TCTCATGTGGCCACCCCGCTGTGAGAGGGCCACAGCACTGACAGCTCACGGCACCGGAGA-	1701
Qy	846	CCCTGGATACCAACAGCTAACCATACAGAGTGGCAGACTATACGATCTGTGGCCCTGGATA	905
Db	1702	-----GCCCTGGATA 1711	
Qy	906	CCAACTACTGCTTCACTGCTCCACGAGAGAACTGCTGTGGCGGACGCTTACATTGACT	965
Db	1712	CCAACTATTGCTTTCAGCTTCCACAGAGAAAGACTGCTGTGGCGGACGCTTACATTGACT	1771
Qy	966	TCCGAAGACCTGGGGCTGGAGTGGATTCAATGAACCCAAAGGCTACATGCCAATTCT	1025
Db	1772	TTAGGAAGACTGGGGTGGAGGTGGATCCACAGGCGCAAGGGCTACCAATGCTTCT	1831
Qy	1026	GCTTGGGGCCCTGTGCTCTACATCTGTGAGGCTTAGACACTAGTACACAGAGTCTTGCTC	1085
Db	1832	GCTGTGGAACCTGGCCCTATATTTTGGAGCTGGACACACAGTACAGCAAGTCTTGGCC	1891
Qy	1086	TGTACACACGACAAACCCGGGCGCTGGCGGCGCCGCTGTCTGCTGCGCAGGCGCTGG	1145
Db	1892	TCTACACACCAACACAAACCGGGCGCTTCCGGCTGCACCGTGTCTGCTGCGCAGGCTTTGG	1951
Qy	1146	AGCCACTGGCCCTGCTGTACTACGTGGGGCGGCAAGGCCAAAGGTGGAGCACTGTGCCAACA	1205
Db	1952	AGCCACTGGCCCTGCTGTACTACGTGGGTGCGCAAGCCCAAGGTGGAGCACTGTGCCAACA	2011
Qy	1206	TGATGTGCGTTCCTGTCAAGTCAAGCTGAGGCCCGCCCGCCCAAGCCCGGCCACC	1265
Db	2012	TGATGTGCGCTCTGTCAAGTCAAGCTGAGGCCCGCCCGCCG-----CCGCGCCTGCC	2065
Qy	1266	GGCAGGCGCGGCGCCACCCCGGCC 1290	
Db	2066	GGCAGGCGCGGCGCCCGCCCGGCC 2090	
RESULT 3			
US-09-948-002-27			
: Sequence 27, Application US/09948002			
: Publication No. US20030050265A1			
: GENERAL INFORMATION:			
: APPLICANT: Nicholas M. Dean			
: APPLICANT: Susan F. Murry			
: TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH			
: FILE REFERENCE: ISPH-0607			
: CURRENT APPLICATION NUMBER: US/09/948,002			
: CURRENT FILING DATE: 2000-09-05			
: PRIOR APPLICATION NUMBER: 09/661,753			
: PRIOR FILING DATE: 2000-09-14			
: PRIOR APPLICATION NUMBER: 60/154,546			
: PRIOR FILING DATE: 1999-09-17			
: NUMBER OF SEQ ID NOS: 71			
: SEQ ID NO 27			
: LENGTH: 1585			

[illegible]

Db 1257 CCAACTACTGCTTCACTCCACAGAGAAGAACTGCTGTGTACGGCAGCTGTACATTGACT 1316
QY 966 TCCGGAAGACCTGGGCTGGAAGTGAATTATCATGAACCAAGGGCTACCATTCATTTCT 1025
Db 1317 TTAGGAAGAACTGGGTGGAGTGTGATCCAGAGGCCCAAGGGCTACCATTCATTTCT 1376
QY 1026 GCGTGGGGCCCTGTCCCTACATCTGGAGCTAGACACTGATGACAGCAAGTCTTGCTC 1085
Db 1377 GTCTGGGGCCCTGCCCCCTACATTTTGGAGCTTGACACACAGTACACAGTCTTGCCCC 1436
QY 1086 TGTAAACAACGACAAACCCGGGGGCGTGGGGGCGCTGTGCTGGGGGCGGCGAGCGCTGG 1145
Db 1437 TCTAAACAACCAACAAACCCGGGGGCTTCCGATCACCGTGTCTGTCGCGAGGCTTTGG 1496
QY 1146 AGCCACTGCCCATGCTACTACTGAGGCGCCGACAGCCCAAGGTGAGAGCTGTCCACA 1205
Db 1497 AGCCACTGCCCATGCTACTACTGAGGCGCCGACAGCCCAAGGTGAGAGCTGTTCACA 1556
QY 1206 TGATCGTGGCTTCTGCAAGTGCAGCTGA 1234
Db 1557 TGATCGTGGCTTCTGCAAGTGCAGCTGA 1585

RESULT 4

US-09-756-283A-19
; Sequence 19, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
; APPLICANT: Chernafovsky, Yuli
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LAP-miFbeta construct
; NAME/KEY: CDS
; LOCATION: (1)..(1368)
US-09-756-283A-19

Query Match 48.1%; Score 654; DB 10; Length 1376;
Best Local Similarity 88.1%; Pred. No. 2,9e-167;
Matches 724; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

QY 11 ATGGCGCCTTGGGGCTGGCGCTCTTTCGGCTGCTGCTGCTGCTGCTGCTAGTG 70
Db 1 ATGGCGCCTTGGGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
QY 71 CTGACGCTTGGCGCGCGCGCGCGGACTGTCACCTGCAAGACCATGACATGAGCTG 130
Db 61 CTGACGCTTGGCGCGCGCGCGCGGACTGTCACCTGCAAGACCATGAGAGCTG 120
QY 131 GTGAAGGGAAGGCGCATGAGGCGCATTTGGCGGCGCATTTCTTCCAGAGCTTGCGCTGCC 190
Db 121 GTGAAGGGAAGGCGCATGAGGCGCATTCGCGGCGCATTCCTTCCAGAGCTTGCGCTGCC 180
QY 191 AGCCCGCGGAGCAGGGGAGTGTGCGCGCGCGGCTGCTGAGGAGTACTGCTGCTT 250
Db 181 AGCCCGCGGAGCAGGGGAGTGTGCGCGCGCGGCTGCTGAGGAGTACTGCTGCTT 240
QY 251 TACAACAGTACCCGCGACCGGGTAGCCGGGAAAGTGTGCAACCGGAGCCGAGCCAGAG 310
Db 241 TACAACAGTACCCGCGACCGGGTAGCCGGGAGAGTGTGCAACCGGAGCCGAGCCAGAG 300
QY 311 GCGGACTACTACGCGCAAGAGAGTCAACCCGCTGTCTAATGTGTGAAGCGGCAACCAAT 370
Db 311 GCGGACTACTACGCGCAAGAGAGTCAACCCGCTGTCTAATGTGTGAAGCGGCAACCAAT 370

Db 301 GCCGACTACTAGCCCAAGAGAGTCAACCCGCGCTGCTAATGTGTGAAGCAACCAAGAAATC 360
QY 371 TATGATTAATTTCAAGGAGCAACCCCAAGAGTATATATGTGTGTCAACAGCTGGAGCTC 430
Db 361 TATGACAAATTTAAGAGAGATACACACAGCATATATATGTTCCTTCAACACATCAAGAGCTC 420
QY 431 CGGGAAGCGGTGCCGGAAGACCTGTATTGCTCTCTCGGGGAGAGAGTGCAGCTGCT--GAGG 487
Db 421 CGAGAAGCGGTACCTGACCAACCCGCTGTGTCTCCGGGAGAGAGTGCCTGCTGAGAGG 480
QY 488 CTCACGTTAAAGTGGAGACGACAGCTGAGACTATACAGAAATACAGATGATTCCTGG 547
Db 481 CTCACGTTAAAGTGGAGACGACAGCTGAGACTATACAGAAATACAGATGATTCCTGG 540
QY 548 GCGTACCTGACGAACCGGCTGCTGGGCCCCAGTACCTCACCGGAGTGGCTGCTTGTAT 607
Db 541 GCGTACCTGACGAACCGGCTGCTGGGCCCCAGTACCTCACCGGAGTGGCTGCTTGTAT 600
QY 608 GTACCCGAGATTGTGGGCAAGTGTGACCCGCGAGAGAGGCTATAGAGGATTTTCGCTC 667
Db 601 GTACCCGAGATTGTGGGCAAGTGTGACCCGCGAGAGGCTATAGAGGATTTTCGCTC 660
QY 668 AGTCCCACTCTTCTCTGACAGCAAAAGATACACACTCCACCTGGAATTAAGGGTTTC 727
Db 661 AGTCCCACTCTTCTCTGACAGCAAAAGATACACACTCCACCTGGAATTAAGGGTTTC 720
QY 728 AATTCGCGCGCGGGGTGACCTGGCCACCATTCACAGGCAATGAACGGCCCTTCTGCTC 787
Db 721 AATTCGCGCGCGGGGTGACCTGGCCACCATTCACAGGCAATGAACGGCCCTTCTGCTC 780
QY 788 CTCATGGCCACCCCGCTGAGAGAGGGCCCAAGACCTGACACAGC 829
Db 781 CTCATGGCCACCCCGCTGAGAGAGGGCCCAAGACCTGACAAAGC 822

RESULT 5

US-09-756-283A-21
; Sequence 21, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
; APPLICANT: Chernafovsky, Yuli
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 1352
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: miFbeta-LAP construct
; NAME/KEY: CDS
; LOCATION: (1)..(1344)
US-09-756-283A-21

Query Match 43.5%; Score 591.4; DB 10; Length 1352;
Best Local Similarity 87.0%; Pred. No. 2,4e-150;
Matches 662; Conservative 0; Mismatches 96; Indels 3; Gaps 1;

QY 73 GACGCTTGGCGCGCGCGCGGACTGTTCACCTGCAAGACCATGACATGAGAGTGGT 132
Db 582 GACGCTTGGCGCGCGCGCGGACTGTTCACCTGCAAGACCATGAGAGTGGT 641
QY 133 GAAGCGGAAGCGCATGAGGCGCATTCGCGGCGAGATTTCTTCCAAAGCTTGCGCTTGCAG 192
Db 642 GAAGCGGAAGCGCATGAGGCGCATTCGCGGCGAGATTCCTTCCAAAGCTTGCGGCTGCAG 701
QY 193 CCCCCGAGCAGGGGAGAGTGCAGCCGCGCGGCTGCTGAGAGCAGTACTGCTCTTTA 252
Db 193 CCCCCGAGCAGGGGAGAGTGCAGCCGCGCGGCTGCTGAGAGCAGTACTGCTCTTTA 252

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Db 702 CCCCCGAGCCAGGGGAGGTGCCGCCGCCGCTGCCAGGCGGTGCTCGCCCTGTA 761
Oy 253 CAACAGTACCCGCGACCGGGTAGCCCGGGGAAAGTGTGAAACGGAGCCGAGCAGAGGC 312
Db 762 CAACAGCACCACCGGACCGGGTGGCCGGGAGAGTGCAGAACCGAGCCGAGCCTGAGGC 821
Oy 313 GGACTACTACGCGCAAGAGGTGACCCCGGTCTAATGTGGAAAAGCGGCAACCAATCTA 372
Db 822 CGACTACTACGCGCAAGAGGTGACCCCGGTCTAATGTGGAAAAGCGGCAACCAATCTA 881
Oy 373 TGAATTAATTCAGAGGCAACCCCGACACTTATATATCTGTTCACACAGTGGAGCTCGG 432
Db 882 TGCACAGTTTCAGAGGCAACCAACACACATATATATCTTCAACACATGAGAGCTCGG 941
Oy 433 GGAAGCGGTGCCGGAACCTGTATTGCTCTCGGGCAGAGCTGGCCCTGCT---GAGGCT 489
Db 942 AGAAGCGGTGATCGAAGCCGCTGTTGCTCTCCCGGCGAGAGCTGCTGCTGAGAGAGCT 1001
Oy 490 CAAGTTAAAGTGGAGCAGACGCTGAGCTATACAGAAATACAGCAATGATTCCTGCGC 549
Db 1002 CAAGTTAAAGTGGAGCAGACGCTGAGCTATACAGAAATACAGCAATGATTCCTGCGC 1061
Oy 550 CTAACTCAGAACCGGCTGTGCTGCCGCCAGTGAATCAGCGAGTGGCTGTCTTGAATGT 609
Db 1062 ATACCTCAGAACCGGCTGTGCTGCCGCCAGTGAATCAGCGAGTGGCTGTCTTGAATGT 1121
Oy 610 CACCGGAGTGTGCGGAGTGTGCTGACCCCGAGAGAGGCTATAGAGGTTTCCGCTCAG 669
Db 1122 CACCGGAGTGTGCGGAGTGTGCTGACCCCGAGAGGCTATAGAGGTTTCCGCTCAG 1181
Oy 670 TGGCCACTCTCTCTGACAGCAAAATTAACACACTCCAGCTGGAATTAACGGGTTCAA 729
Db 1182 CGCCCACTCTCTCTGACAGCAAAATTAACACACTCCAGCTGGAATTAACGGGTTCAA 1241
Oy 730 TTTGCGCCCGCGGGGAGCTGCGCACCATTCACGGGATGAAACGGCCCTTCCGCTGCT 789
Db 1242 TACCGGCGCGCGAGGAGTGTGCTGCGCACCATTCATGCGATGAAACGGCCCTTCCGCTGCT 1301
Oy 790 CATGGCCACCCCGCTGAGAGAGGCGCCAGCACCTGCACAGCT 830
Db 1302 CATGGCCACCCCGCTGAGAGAGGCGCCAGCACCTGCACAGCT 1342

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RESULT 6

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; Sequence 1, Application US/09813271B
; Patent No. US20020115834A1
; GENERAL INFORMATION:

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APPLICANT:
TITLE OF INVENTION: (A) NICO Cerletti
                biologically active protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: No. US20020115834A1artis Patent Department
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,271B
FILING DATE: 20-Mar-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02719
FILING DATE: 12-Jul-95
APPLICATION NUMBER: EPO 94810439.3
FILING DATE: 25-Jul-94

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ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hessa J.
REGISTRATION NUMBER: 22640
REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6940
TELEFAX: (908) 522-6955
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.hTGF-beta1 (DSM 5656)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product= "human TGF-beta1"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-813-271B-1

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Query Match      22.7% Score 308.6; DB 10; Length 339;
Best Local Similarity 94.4%; Pred. No. 4,7e-74;
Matches 320; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Oy 896 GCCCTGGATACCACTACTGCTTCACGCTCCAGGAGAGAACTGCTGCGGACGCTC 955
Db 1 GCCCTGGAGACCACTATTGCTTCACGCTCCAGGAGAACTGCTGCGGACGCTG 60
Oy 956 TACATTGACTTCGGAAGAGACCTGGGCTGGAGTGGATTCATGACCAAGGCTACCAT 1015
Db 61 TACATTGACTTCGGAAGAGACCTGGGCTGGAGTGGATTCATGACCAAGGCTACCAT 120
Oy 1016 GCCAATTCCTGCGTGGGCGCTGCTCCCTACATCTGAGGCTAGACACTAGTACAGCAAG 1075
Db 121 GCCAATTCCTGCGTGGGCGCTGCTCCCTACATCTGAGGCTAGACACTAGTACAGCAAG 180
Oy 1076 GTCCGTGGCTGTATACACAGCAGAACCCGGGCGCTCGGCGGCGCGCTGCTGCTGCGG 1135
Db 181 GTCCGTGGCTGTATACACAGCAGAACCCGGGCGCTCGGCGGCGCGCTGCTGCTGCGG 240
Oy 1136 CAGGCGCTGGAGCCGCTGCCATCGTGTACTAGCTGAGGCGGCAAGGCCAAGGTGGAGCAG 1195
Db 241 CAGGCGCTGGAGCCGCTGCCATCGTGTACTAGCTGAGGCGGCAAGGCCAAGGTGGAGCAG 300
Oy 1196 CTGTCCACATGATGCTGCGTTCCTGCAAGTGCAGCTGA 1234
Db 301 CTGTCCACATGATGCTGCGTTCCTGCAAGTGCAGCTGA 339

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RESULT 7

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US-10-028-158-20
; Sequence 20, Application US/10028158
; Patent No. US20020110833A1
; GENERAL INFORMATION:
APPLICANT: Caniglia, Isabella
APPLICANT: Post, Martin
TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
TROPICOBLAST
CURRENT REFERENCE: 1175.38USMO
CURRENT APPLICATION NUMBER: US/10/028,158
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US/09/380,662
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: PCT/CA98/00180
PRIOR FILING DATE: 1998-03-05
PRIOR APPLICATION NUMBER: US 60/039,919
PRIOR FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 24

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Ob 1092 TCATGATGATTCCCCC

IMMEDIATE SOURCE:
C1ONE: F C014 TC137/bPLM). TGF-beta1(44/45)beta3

DESCRIPTION: /desc = recombinant hybrid DNA of
IMMEDIATE SOURCE: .

CLONE: E. coli LC137/pPLMu.TGF-beta1(44/45)beta3

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? FEATURE:
? NAME/KEY: mat.peptide
? LOCATION: 1..132
? OTHER INFORMATION: /product= "N-terminal 44 amino
? acids of human TGF-beta1"
?
? FEATURE:
? NAME/KEY: mat.peptide
? LOCATION: 133..336
? OTHER INFORMATION: /product= "C-terminal 68 amino
? acids of human TGF-beta3"
?
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..336
? OTHER INFORMATION: /product= "hybrid TGF-beta named
? TGF-beta1-3"
?
? SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
IS-09-813-271B-7

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	Query Match	16.7%	Score 227.2	DB 10	Length 336	
	Best Local Similarity	79.8%	Pred. No. 4.6e-52			
	Matches 268	Conservative	0	Mismatches 66	Indels	Gaps
Qy	896	GCCCTGGATACCAACTACTGCTTCAAGTCCACGAGAAAGAACTGCTGCGTGGGAGCTC	955			
Db	1	GCCCTGGACACCAACTATTGCTTCAAGTCTCCAGGAGAAAGAACTGGCTGCGTGGGAGCTG	60			
Qy	956	TACATTGACTTCGGGAAGAGACCTGGGCTGGAGAGTGATTTATGAAACCCAAAGGCTTACCT	1015			
Db	61	TACATTGACTTCGGCAAGAGACCTCGGCTGGAGAGTGATTCACAGAGCCCAAGGCTTACAT	120			
Qy	1016	GCCATTTCCTGCTGGGGCGCTGCTCCCTCACTGGAGAGCTTGAGACTCAGTAAACAGCAAG	1075			
Db	121	GCCACTTCCTGCTCAGGGCCCTTGGCCCATACCTCCGAGTGCAGACACCAACCACAGCAG	180			
Qy	1076	GTCCTGGCTCTGTACAAACAGCAACACCGGGCGCTCGGCGGCGGCTGTCTGCTGCCG	1135			
Db	181	GTGCTGGGACTGTACAAACACTGTGAAACCTGGAAGCATCTGCGCTTGTGCTGCGTCC	240			
Qy	1136	CAGGCGCTGGAGGCACTGCCATCTGTATCACTGTGGGCGGCAAGCCCAAGTGGAGCAG	1195			
Db	241	CAGGACCTGGAGGCCCTGCACCACTCCGTACTATGTTGGGAGGAGCCCCCAAAAGTGAGCAG	300			
Qy	1196	CTGTCCAACTGATGCTGGCTGCTCCCAAGTAGC	1231			
Db	301	CTCTCCACATGGTGTGAAGTCTTTTAATGTAGC	336			

RESULT 9
 US-09-813-271B-5
 Sequence 5, Application US/09813271B
 Patent No. US20020115834A1
 GENERAL INFORMATION:
 APPLICANT:
 (A) NICO CERJELLETI
 TITLE OF INVENTION: New process for the production of
 biologically active protein
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. US20020115834A1artis Patent Department
 STREET: 564 Morris Avenue
 CITY: Summit
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07901
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION NUMBER: US/09/813, 271B
 APPLICATION NUMBER: 20-Mar-2001
 FILING DATE: 20-Mar-2001
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/02719
FILING DATE: 12-Jul-95
APPLICATION NUMBER: EPO 94810439.3
FILING DATE: 25-Jul-94
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Henna J.
REGISTRATION NUMBER: 22640
REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/JUSN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6940
TELEFAX: (908) 522-6955
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.hTGF-beta3 (DSM 5658)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product= "human TGF-beta3"
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Query Match	15.4%	Score 209.4	DB 10	Length 339
Best Local Similarity	76.1%	Pred. No. 3e-47		
Matches 258	Conservative	0	Mismatches 81	Indels 0
				Gaps
Qy 896	GGCCGCGATACCAACTACGCTTCACCTCCACGAGAGAAGTGCCTCGCGGACGCTC	955		
Db 1	GGTTTGGAAACCAATTACTCTCTCCGCAACTTTGGAGAGAACTGCTGTGCGCCCTTC	60		
Qy 956	TACATTGACTTCCGGAAGACCTGGGCTGGAAGTGAATCATGAGACCAAGGCTACCAT	1015		
Db 61	TACATTGACTTCCGAGACGAAATGTGGGCTGGAAAGGCTGCATGAACTTAAGGGTACTAAT	120		
Qy 1016	GCCAAATTTTGCCTGGGGGCCCTTCCTTACATCTGGAGGCTAGACACTCAGTAGAGCAAG	1075		
Db 121	GGCAACTTTCGCTCAGGGCCCTTGCCCACTACTCCGCAAGTGACACACCAACCAAGACAGC	180		
Qy 1076	GTCCTGGACTGTACAAACAGACACAAACCCGGGCGCGCTCGGCGGCGCGCTGCTGCGTGGCC	1135		
Db 181	GTCTGTGGACTGTACAAACTCTGAAACCTTGAAACATCTGCTGGCTTGGCTGGCTGCC	240		
Qy 1136	CAGGCGCTGAGGCCACTGCCCAATGCTGTACTAGCTGGGCCCAAGCCCAAGTGGAGCAG	1199		
Db 241	CAGGACTGTGAGCCCTGACCACATCTGTACTATGTTTGGAGGAGACCCCAAGTGGAGCAG	300		
Qy 1196	CTGTCCAACTGATCGTGGCTTCTCGAAGGCAAGCTGA 1234			
Db 301	CTCTCCAACTGGTGGTAAGTCTTGTAAATGTAGCTGA 339			

RESULT 10
 US-09-813-271B-11
 ; Sequence 11, Application US/09813271B
 ; Patent No. US20020115834A1
 ;
 GENERAL INFORMATION:
 ;
 APPLICANT:
 ; (A) Nico Cerletti
 ;
 TITLE OF INVENTION: New process for the production of
 ;
 ; biologically active protein
 ;
 ;
 NUMBER OF SEQUENCES: 13
 ;
 ;
 CORRESPONDENCE ADDRESS:
 ;
 ; ADDRESSSEE: No. US20020115834A1artis Patent Department
 ;
 ;
 CITY: Summit
 ;
 ;
 STATE: New Jersey
 ;
 ;
 COUNTRY: USA
 ;
 ;
 ZIP: 07901
 ;
 ;

Db 1 GCTTTGGATCGGGCTATTGCTTTAGAAATGTGAGAGATAATGCTGCTACGTCCACT 60
Qy 956 TACATTGACTTCCGGAAGAGACTGGGCTGGAGTATTCAGAACCAAGGGTACCAT 1015
Db 61 TACATTGATTCAAGAGGAGTCTAGGGTGGAAATGATACGACCAACCAAGGCTACAT 120
Qy 1016 GCCAATTTTGGCTGGGGCCCTGTCCCTACATCTGAGACCTGACACTAGTAGCAAG 1075
Db 121 GCCAATTTTGGCTGGGGCCCTGTCCCTACATCTGAGACCTGACACTAGTAGCAAG 180
Qy 1076 GTCTGGCTCTGTAGCAACCAAGCAACACCGGGGCGGCGGGGCGGCTGCTGGTGGC 1135
Db 181 GTGCTGGAGCTGTACACACTGTGAACTGAAACCTGAAACATCTGCTGCTGCTGCTG 240
Qy 1136 CAGGCGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1195
Db 241 CAGGAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Qy 1196 CTTGTCCAACTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
Db 301 CTTGTCCAACTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 336

RESULT 12

Sequence 47, Application US/09948002
Publication No. US20030050265A1
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Susan F. Murray
TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
FACTOR BETA EXPRESSION
FILE REFERENCE: ISPH-0607
CURRENT APPLICATION NUMBER: US/09/948,002
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 09/661,753
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/154,546
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 47
LENGTH: 4267
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (1218)...(2462)
US-09-948-002-47

Query Match 13.2% Score 179.8: DB 9: Length 4267;
Best Local Similarity 51.9% Pred. No. 3,4e-39;
Matches 635; Conservative 0; Mismatches 532; Indels 56; Gaps 8;

Qy 69 TCGTGAACGCTGGCG 128
Db 1249 TCGTGAACGCTGGCG 1308
Qy 129 TGTGTACAGCGAAGCGGATCGAGCGCATTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 188
Db 1309 AGTTTATCGGAAGAGAGTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
Qy 189 CCAGCG 248
Db 1369 CCAGCG 1425
Qy 249 TTTACACAGTACCG 296
Db 1426 TCTACACAGTACCG 1485
Qy 297 AGCG 356
Db 1486 AGCG 1545

Qy 357 GCGGACCAACAAATCTATGATTAATTCAGGCAACCCCGACAGCTTATATGCTGTCA 416
Db 1546 CCGACCTCCCTCCCGAAATGCGCATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1605
Qy 417 ACAGCTGGAGGCTCCGGAAGCGGTCGCGGAACTGTATGCTCTCTCGGAGAGCTG- 475
Db 1606 TCGGCTTATGATCTCAACATGAGAGAAATGCTTGTGATCTGTGTGAGAGAGTCA 1665
Qy 476 -----CGCTGCTGAGGCTCAAGTTAAAGT---GAGCAGCAGTGGAGCTATACC 524
Db 1666 GGGCTTCGCTTGGCAAAACCCCGAAAGCCAGAGTGGCGCGGAGGAGGATGATGATC 1725
Qy 525 AGA-----AATACAGCAATGATTCGCGGCTACCTCAGAGACCGGCTGC 569
Db 1726 AGATCTTAAATCCAAAGCTTATACATCTCCACCGAGGCTACATGATGATGAGAGGTTG 1785
Qy 570 TGGCCCCAGTACCTACCGAGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 629
Db 1786 TGAAGACAGAGCGGAGGAGTGAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1845
Qy 630 GGGTACCGCGAGAGAGGCTATAGAGGTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 689
Db 1846 GGGTTCACCAACAAAGAGAGAGGAGGCTTAAATTAAGTTTACCTGCGCTGTGA 1905
Qy 690 GC-----AAAGTAAACACACCTCCAGTGGAAATTAAGGGTCAATTCTGGCC 737
Db 1906 CTTTGTGCTGCTGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1965
Qy 738 GCGGCGGTGACCTGCGCACCATTCACGAGCATGACCGCGCGCTTCTGCTGCTGCTGCTG 797
Db 1966 TTGAGGATATGATGACCTTACATATGATGATGATGATGATGATGATGATGATGATGAT 2025
Qy 798 CCGCGCTGGAGAGGCG 856
Db 2026 CTAGGAAAAAAGCAGTGGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2085
Qy 857 AACAGCTACCCATACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 916
Db 2086 GAGTGGAGTCAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2144
Qy 917 TTTGAGCTCCAGGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 976
Db 2145 TTTGAGAGATGAGAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2204
Qy 977 CTGGGCTGGAAGTGGATTCAGAAACCAAGGCTACCATGCAATTTCTGCTGCGCGCGCG 1036
Db 2205 CTTGAGTGAAGATGATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2264
Qy 1037 TGTCCCTACATCTGAGGCTGTAGACACTGATGATGATGATGATGATGATGATGATGATG 1096
Db 2265 TGCCCATATCTATGAGGAGTTCAGACACTCAACACCAAGTCTCAGGCTGTACCAACAC 2324
Qy 1097 CACAAACCGGCGCGCTGCG 1156
Db 2325 ATAAATCCCGAAGCTTCGCTTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2384
Qy 1157 ATCTGTACTACGTGGGCGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1216
Db 2385 ATCTGTACTATGATGAGAAATACCGCGCAAGATGATGATGATGATGATGATGATGATG 2444
Qy 1217 TCTGTGCAAGTGTGAGGCGC 1239
Db 2445 TCTGTGTAATGTCAAGTAAAGTCC 2467

RESULT 13

US-09-813-271B-3
Sequence 3, Application US/09813271B
Patent No. US20020115834A1
GENERAL INFORMATION:
APPLICANT: (A) Nico Cerletti
TITLE OF INVENTION: New process for the production of

biologically active protein

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: No. US20020115834A1artis Patent Department
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,271B
FILING DATE: 20-Mar-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02719
FILING DATE: 12-Jul-95
APPLICATION NUMBER: EPO 94810439.3
FILING DATE: 25-Jul-94
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Henna J.
REGISTRATION NUMBER: 22640
REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6940
TELEFAX: (908) 522-6955
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.hTGF-beta2 (DSM5657)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product="human TGF-beta2"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-813-271B-3

Query Match 11.6%; Score 158.2; DB 10; Length 339;
Best Local Similarity 66.7%; Pred. No. 2.1e-33;
Matches 226; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

896 GCCCTGATACCAACTACTGCTTCAGTCCAGAGAGAACTGCTGCGGCGAGCTC 955
1 GCTTTGGATGGGCGCTATTGCTTGAATGTCAGAGAAATGCTGCGCTACCTC 60
956 TACATTGACTTCCGGAAGACCTGGGCTGGAAGTATTCATGAAACCAAGGCTACAT 1015
61 TACATGATTTCAAGAGGATCTAGAGGTGAATGATACAGAAACCAAGGTTCAAT 120
1016 GCCAATTTCTGCGGCGGCGCTGACATCTGAGGCTGAGCACTAGTACAGCAAG 1075
121 GCCCACTTCTGCTGGAGCATAGCCGATTTATGAGATTCAAGACACTACAGCAGAG 180
1076 GTCTGCTCTGTACACACACACACCGGCGGCTGCGGCGGCGCTGCTGCGG 1135
181 GTCTGAGCTTATATATATACATATCAAGAAAGATCTGCTTCTCTGCTGCTGCTC 240
1136 CAGGCGCTGAGACCACTGCCATCTGATCTACGTGGCGGCGCAAGCCCAAGTGGAGCAG 1195
241 CAAGATTTAGAACCTTACCACTATCTCTACTACTGCAAAACACCAAGATTGAACAG 300
1196 CTGTCAACATGATGCTGCTCTGCAAGTGAAGCTGA 1234
301 CTTTCTAATATGATTGTAAGTCTTGCAATGACGCTAA 339

RESULT 14
US-10-044-090-323
Sequence 323, Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 323
LENGTH: 2912
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 3146342CB1
US-10-044-090-323

Query Match 11.6%; Score 158.2; DB 12; Length 2912;
Best Local Similarity 66.7%; Pred. No. 3.4e-33;
Matches 226; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

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1604 GCTTTGGATGGGCGCTATTGCTTGAATGTCAGAGAAATGCTGCGCTACCTC 1663
956 TACATTGACTTCCGGAAGACCTGGGCTGGAAGTATTCATGAAACCAAGGCTACAT 1015
1664 TACATTGATTTCAAGAGGATCTAGGAGTAATGATACAGAAACCAAGGTTCAAT 1723
1016 GCCAATTTCTGCGGCGGCGCTGACATCTGAGGCTGAGCACTAGTACAGCAAG 1075
1724 GCCAATTTCTGCTGGAGCATAGCCGATTTATGAGATTCAAGACACTACAGCAGAG 1783
1076 GTCTGCTCTGTACACACACACCGGCGGCTGCGGCGGCGCTGCTGCTGCTGCGG 1135
1784 GTCTGAGCTTATATATATACATATCAAGAAAGATCTGCTTCTCTGCTGCTGCTC 1843
1136 CAGGCGCTGAGACCACTGCCATCTGATCTACGTGGCGGCGCAAGCCCAAGTGGAGCAG 1195
1844 CAAGATTTAGAACCTTACCACTATCTCTACTACTGCAAAACACCAAGATTGAACAG 1903
1196 CTGTCAACATGATGCTGCTCTGCAAGTGAAGCTGA 1234
1904 CTTTCTAATATGATTGTAAGTCTTGCAATGACGCTAA 1942

RESULT 15
US-09-864-761-15319/c
Sequence 15319, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aemica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04

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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 15319
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011462.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.8
US-09-864-761-15319

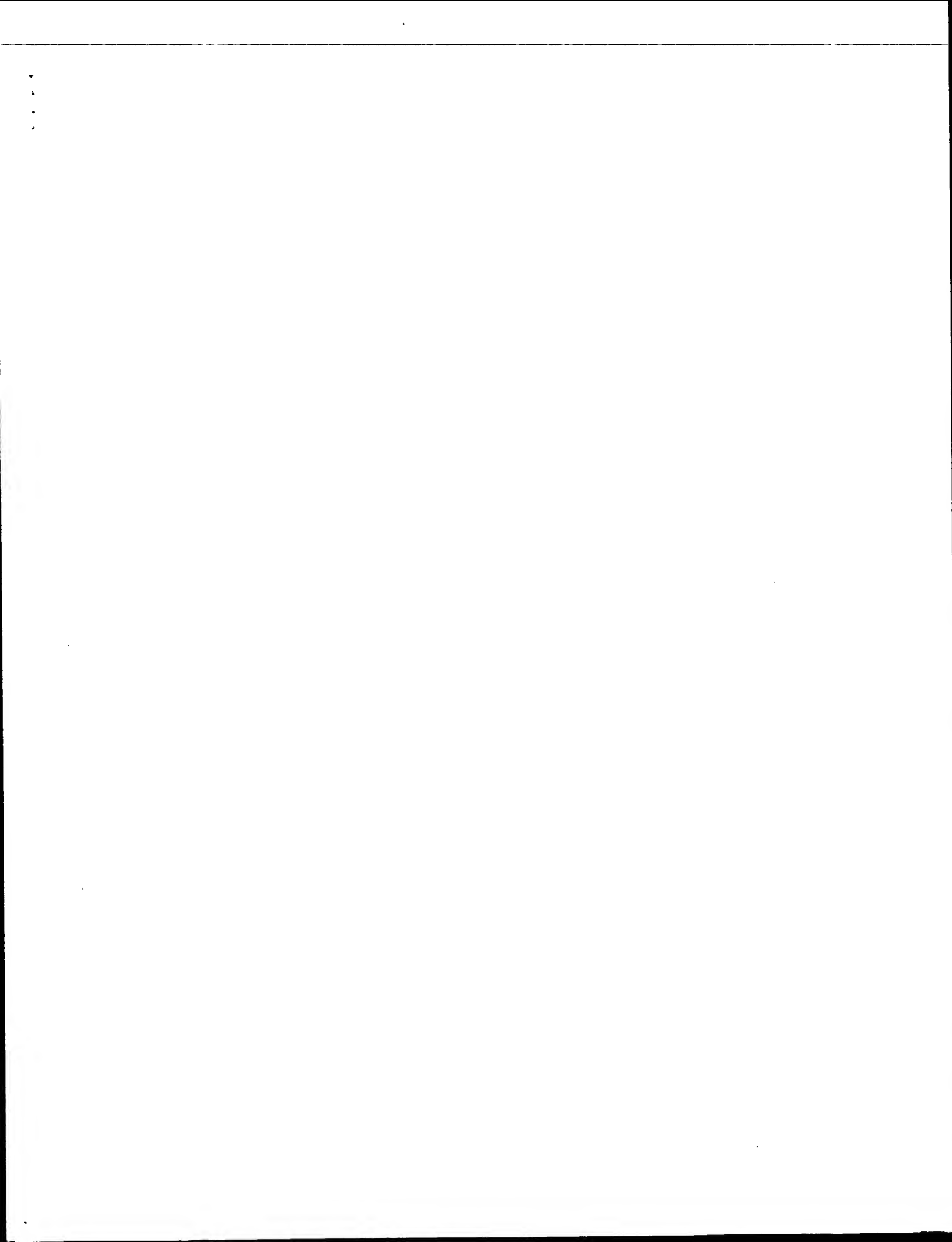
Query Match      10.4%; Score 141.6; DB 10; Length 597;
Best Local Similarity 91.5%; Pred. No. 7,3e-29;
Matches 150; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 916 CTTGAGCTCAGAGAGAGAACTGCTGCGGCGGAGCTCTACATGACTTCGGGAAGA 975
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Db 458 CTGAGGCTCAGAGAGAGAACTGCTGCGGCGGAGCTCTACATGACTTCGGGAAGA 399
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 976 CCTGGGCTGGAAGTGTGATTCATGAACCAAGGGCTACCAATGCCAATTTCTGCTGGGGCC 1035
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 398 CCTGGGCTGGAAGTGTGATTCATGAACCAAGGGCTACCAATGCCAATTTCTGCTGGGGCC 339
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 1036 CTGTCCCTACATCTGGAGCTAGACATCAGTACAGCAGAGTCC 1079
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 338 CTGCCCCCTACATTGTGAGCTGGACACGCGATCAGCAGAGGTAC 295
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Search completed: April 15, 2003, 11:57:16
Job time : 206 secs



GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 10:09:10 ; Search time 2186 seconds
(without alignments)
10083.283 Million cell updates/sec

Title: US-10-017-372e-36

Perfect score: 1361

Sequence: 1 cgtacagagatgcgcctt.....cgattaagcgccgcgact 1361

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :
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2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gp_estl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	703.6	51.7	1072	13	BM562135
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3	577.4	42.4	789	9	AL530081
4	570.6	41.9	713	10	BE312000
5	562.6	41.3	717	10	BE260971
6	562	41.3	902	14	BQ675698

7	534.4	39.3	925	13	BT188841
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12	506.6	37.2	1093	14	BM469326
13	504.8	37.1	943	13	BM054305
14	502	36.9	821	12	BT909079
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20	459.8	33.8	637	13	AT148173
21	455.8	33.5	748	13	BM938856
22	455.4	33.5	814	12	BF682938
23	452.2	33.2	548	13	BM686959
24	450	33.1	982	14	BM068788
25	447.6	32.9	981	14	BQ672677
26	446	32.8	659	12	BM802192
C	27	444.6	32.7	778	9
C	28	443.6	32.6	1015	12
29	442.4	32.5	636	10	BE683840
30	441.6	32.4	599	13	BE615330
31	435	32.0	821	10	BT905963
32	434.4	31.9	1228	14	BE311897
C	33	432	31.7	676	14
C	34	426	31.3	660	13
C	35	425.8	31.3	664	9
C	36	425	31.2	662	14
37	423.2	31.1	943	14	BM0576225
C	38	421.6	31.0	678	14
C	39	418.6	30.8	660	14
40	416.4	30.6	1028	14	BQ018647
41	411.8	30.3	540	13	BQ670359
42	411.4	30.2	719	14	BT834732
C	43	409.6	30.1	654	14
C	44	408.8	30.0	639	12
45	406.2	29.8	869	14	BF723491

ALIGNMENTS

RESULT 1
BM562135
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM562135 1072 bp mRNA linear EST 20-FEB-2002
AGENCOURT_6562032 NTH_MGC_118 Homo sapiens CDNA clone IMAGE:5745463
5', mRNA sequence.
BM562135.1 GI:18807966
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1072)
NTH-MGC http://mgs.nci.nih.gov/
Unpublished (1999)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
http://image.llnl.gov
plate: ILAMI2768 row: h column: 08
High quality sequence start: 9
High quality sequence stop: 647.
Location/Qualifiers

FEATURES


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OY 396 ACAGCTTATATATGCTTCAACAGCTCGAGCTCCGGGAAGCGGTGCCGAACCTGTAT 455
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Db 1 ACAGCATATATATGTTCTTCAACATCAGAGCTCCGAGAAGCGGTACTGAAACCCGTGT 60
OY 456 TGTCTCTGCGGAGAGAGCGCGCTGTGTAGGGCTCAAGTTAAAGTGGAGCAGACGG 515
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Db 61 TGTCTCTCCGGGAGAGAGTGTGTGTGTAGGGCTCAAGTTAAAGTGGAGCAGACGG 120
OY 516 ACCTATACAGAAATACAGCAATGATCTCTGCGGCTACCTCAGCAACCGGTGTGGGCC 575
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ACCTATACAGAAATACAGCAATGATCTCTGCGGCTACCTCAGCAACCGGTGTGGGCC 180
OY 576 CCAGTACTACCGGAGTGGCTCTCTTATATGTACCGAGATTGTCCGGCAGTGGCTGA 635
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Db 181 CCAGCAGCTCCGCGAGAGTGTATCTTTTATGTATCACCAGATTGTCCGGCAGTGGTGA 240
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OY 696 AATAACACACTCCACGTGGAATTAACGGGTTCAATTCTGCGCGCGGGTGACCTGGCCA 755
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Db 361 CCATTATGATGATGAACCGGCCCTTCTCTCTCTCATGTGCCACCCCGCTGGAGAGGGCC 420
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Db 421 ACATCTGTGAAGCTCTCCGGCACCGCGCA----- 449
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Db 450 -----GCCCTGGACACCAACTTGTGCTTACGCTCCACGGAGAGA 489
OY 936 ACTGCTGCTGCGGAGAGCTCTTACATTGACTTCCGGAAGACCTGGGCTGGAAGTGATTC 995
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Db 490 ACTGCTGCTGCGGAGAGCTGTACATTGACTTCCGGAAGACCTGGGCTGGAAGTGATTC 549
OY 996 ATGAACCCCAAGGGCTACCATTTCTGCTGGGCGCTGTCTTACATCTTGAGACC 1055
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 550 ACGAGCCCAAGGGCTACCATTTCTGCTGGGCGCTGTCTTACATTTTGAGACC 609
OY 1056 TAGACACTGATACAGCAAGTCTGCTGTGTACAACAGCAACCCGGGCGCGTCCG 1115
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 610 TGGACACGAGTACACAGAGTCTGTGCTGTGTACAACAGCAACCCGGGCGCGTCCG 669
OY 1116 CGGCGCGCTGTGCTGTGCGGAGAGCGCTGGAGCCACTGCCATGCTGTACTACGTGGCC 1175
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Db 670 CGGCGCGCTGTGCTGTGCGGAGAGCGCTGGAGCCGCTGCCATGCTGTACTACGTGGCC 729
OY 1176 GGAAGCCCAAGGGTGGAGAGCTGTCCAATGATCTGCTGTCTGTGCAAGTGCAGCTGAG 1235
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Db 730 GGAAGCCCAAGGGTGGAGAGCTGTCCAATGATCTGCTGTCTGTGCAAGTGCAGCTGAG 789
OY 1236 GCCCGCGCGCGCGCACAGCGCGCGCACCGCGGAGCGCGCCGCGCGCGCGCGCTC 1295
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 790 GGGTCCGCGCGCGCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 849
OY 1296 ACCGGGG 1302
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Db 850 GGGCGGG 856
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RESULT 3
LOCUS AL530081 789 bp mRNA linear EST 13-FEB-2001
DEFINITION AL530081 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD009YK06 5
prime, mRNA sequence.
ACCESSION AL530081
VERSION AL530081.1 GI:12793574
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KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM human.
REFERENCE 1 (bases 1 to 789)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
CONTACT Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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            /db_xref="taxon:9606"
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            /clone_11b="LTI_NFL001_NBC4"
            /sex="male"
            /tissue_type="neuroblastoma cells"
            /lab_host="DH10B"
            /note="organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by life technologies. Contact : Feng Liang life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@life.techn.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 159 a 254 c 240 g 134 t 2 others
ORIGIN
Query Match 42.4%; Score 577.4; DB 9; Length 789;
Best Local Similarity 87.0%; Pred. No. 6,9e-116;
Matches 643; Conservative 2; Mismatches 93; Indels 1; Gaps 1;

OY 6 CCGAATGGCGGCTTCGGGGCTGCGGCTCTTGGCGCTGTGCTGCTGCCGCGCTGTGCTGC 65
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Db 51 CCCCAGTGGCGGCTTCGGGGCTGCGGCTCTTGGCGCTGTGCTGCTGCTGCTGCTGCTGCTAC 110
OY 66 TAGTCTGACGCGCTGCGCGCGCGCGCGCGGAGCTGTCACTCTCAAGACCATGACATGG 125
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Db 111 TGTGTCTGACGCGCTGCGCGCGCGCGCGCGGAGCTATCCACTCTCAAGACTATGACATGG 170
OY 126 AGCTGTGAGCGGAAGCGCATCGAGGCCATTGCGCGCGCAGATTCTGTCCAAGCTTGGC 185
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Db 171 AGCTGTGAGCGGAAGCGCATCGAGGCCATCGAGGCCATCGCGCGCAGATCTGTCCAAGCTGCGGC 230
OY 186 TTGGCAGCGCGCGCGCGCGGAGGAGGAGTGCCTCCCGCGCGCGCGCGCTGTGAGAGCACTGG 245
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Db 231 TCGCAGCGCGCGCGCGCGGAGGAGTGCCTCCCGCGCGCGCGCGCGCGCGCTGTG 290
OY 246 CTCTTTAACAACAGTACCGCGCGCGGAGTGCAGGAGGAGGAGTGTGCAAGCGGAGCGCGAGC 305
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Db 291 CCTGTACAACAGCAACCGCGGAGCGCGGAGGAGTGTGCAAGGAGGAGCGCGAGC 350
OY 306 CAGAGCGGAGTACTACGCGCGCAAGAGAGTCAACCGCGGTGTATGTGTGGAAGCGGCAACC 365
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Db 351 CTGAGCGCGAGTACTACGCGCGCAAGAGAGTCAACCGCGGTGTATGTGTGGAAGCGGCAACC 410
OY 366 AAATCTATGATTAATTAATTAAGGAGCGACCGCGCGCAAGTATATATGCTTCAACAGCTCGG 425
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Db 411 AAATCTATGACAGTATTAAGAGAGTACACAGCATATATATATGTTCTTCAACAGCTCAG 470
OY 426 AGCTCCGGAAGCGGTTGCCGGAAGCTGTATGCTCTCTCTGCGGAGAGAGCTGCGCGCTGTGA 485
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Db 471 AGCTCCGGAAGCGGTTACTGAAACCGGTGTCTCTCTGCGGAGAGAGCTGCGCTGTGTGA 530
OY 486 GGCTCAAGTTAAAGTGGAGCAGCACGTGGAGCTATACAGAAATACAGCAATGATTTCTT 545
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Db 531 GGCTCAAGTTAAAGTGGAGACACAGCTGTACAGAAATACAGCAATTCCT 590
 Oy 546 GGGCTACTCTACAGAACCGGCTCTGGCCCCCACTACTACCCGAGAG -GCTGCTCTT 604
 Db 591 GGGCTACTCTACAGAACCGGCTCTGGCCCCCACTACTACCCGAGAG -GCTGCTCTT 650
 Oy 605 GATGTCACCGGAGTTGTGGGCGAGTGGTACCCGACAGAGAGGCTATAGAGGTTTTCGC 664
 Db 651 GATGTCACCGGAGTTGTGGGCGAGTGGTACCCGACAGAGAGGCTATAGAGGTTTTCGC 710
 Oy 665 CTCAGTCCCACTCTTCTCTGACAGCAAGATACACACTCCACGTTGAATTAACGGG 724
 Db 711 CTYACGCCACCTACTCTCTGTGACAGCGAGGATTAACACTGCAATGACATCAACGGG 770
 Oy 725 TTCAATTCGCGCGCGGG 743
 Db 771 TTCTACTACCGCGCGCGAG 789

RESULT 4
 BE312000 713 bp mRNA linear EST 26-OCT-2000
 LOCUS 601154768F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3510592 5',
 DEFINITION mRNA sequence.
 ACCESSION BE312000
 VERSION BE312000.1 GI:9130128
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 713)
 NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: L1CM193 row: h column: 17
 High quality sequence start: 2
 High quality sequence stop: 713.

FEATURES

Source

1..713
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3510592"
 /clone_lib="NIH_MGC_19"
 /tissue_type="neuroblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; CDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 157 a 226 c 211 g 119 t
 ORIGIN

Query Match 41.9%; Score 570.6; DB 10; Length 713;
 Best local similarity 87.5%; Pred. No. 2.1e-14;
 Matches 624; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

Oy 135 AGCGAAGCGATCGAGCGCATTCGCGGCGAGATCTGTCCAACTGCGGCTGCCAGCC 194
 Db 1 AGCGAAGCGATCGAGCGCATTCGCGGCGAGATCTGTCCAACTGCGGCTGCCAGCC 60

Oy 195 CCCCAGACAGAGGGAGAGTCCGCCGCCGCTGCTGAGCGAGTACTCTTTACA 254
 Db 61 CCCGAGACAGAGGGAGAGTCCGCCGCCGCTGCTGAGCGAGTACTCTTTACA 120
 Oy 255 ACAGTACCCCGGAGCCGGGTACCCGGGGAAGTGTGTGAACCCGAGCCGAGAGCGG 314
 Db 121 ACAGACCCCGGAGCCGGGTACCCGGGGAAGTGTGTGAACCCGAGCCGAGAGCGG 180
 Oy 315 ACTACTACGCCAAGAGAGTCAACCCGCTGCTTAATGTTGGAAGAGCGGCAACAATCTATG 374
 Db 181 ACTACTACGCCAAGAGAGTCAACCCGCTGCTTAATGTTGGAAGAGCGGCAACAATCTATG 240
 Oy 375 ATAAATTCAGAGGCAACCCCAAGTATATATCTGTTCACACAGTGGAGCTCCGGG 434
 Db 241 ACAAGTTCAACGACAGATGACACAGCATATATATGTTCTTCAACACATCAGAGCTCCGAG 300
 Oy 435 AAGCGGTCCCGAACCCTGATCTCTCCGCGGAGAGCTGGCCGCTGAGGCTCAAGT 494
 Db 301 AAGCGGTACCTGAACCCGCTGCTCTCCGCGGAGAGCTGGCCGCTGAGGCTCAAGT 360
 Oy 495 TAAAGTGGAGACAGCAGCTGAGCTATACAGAAATACAGCAATGATTCCTGGCGTACC 554
 Db 361 TAAAGTGGAGACAGCAGCTGAGCTATACAGAAATACAGCAATGATTCCTGGCGTACC 420
 Oy 555 TCAGCAACCGGCTGCTGACCCCAAGTACTACCGGAGTGTCTTGTATGTACCG 614
 Db 421 TCAGCAACCGGCTGCTGACCCCAAGTACTACCGGAGTGTATCTTTGATGTACCG 480
 Oy 615 GAGTTGCGGCGAGTGGCTGACCCGAGAGAGCTATAGAGGTTTGGCTCAGTCCG 674
 Db 481 GAGTTGCGGCGAGTGGCTGACCCGAGAGAGCTATAGAGGTTTGGCTCAGTCCG 540
 Oy 675 ACTTCTCTGTACAGCAAGATTAACACACTCCAGCTGGAATTAACGGGTTCAATTCG 734
 Db 541 ACTGCTCTGTGACAGCAGGAGTAAACACTGCAAGTGAACATCAACGGGTTCACTACCG 600
 Oy 735 GCCCGCGGGGTGACTGGCCACCATTCACAGGATGAACCGCCCTTCCTCTCATAGG 794
 Db 601 GCCCGCGGGGTGACTGGCCACCATTCACAGGATGAACCGCCCTTCCTCTCATAGG 660
 Oy 795 CCACCCCGCTGGAGAGGCGCCAGCACTGCGGAGAGTCCCGGCGAGCGGCC 847
 Db 661 CCACCCCGCTGGAGAGGCGCCAGCACTGCGGAGAGTCCCGGCGAGCGGCC 713

RESULT 5
 BE260971 717 bp mRNA linear EST 26-OCT-2000
 LOCUS 601153715F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509921 5',
 DEFINITION mRNA sequence.

ACCESSION BE260971
 VERSION BE260971.1 GI:9132709
 KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 717)
 NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: L1CM193 row: m column: 04
 High quality sequence stop: 713.

FEATURES

Source

1..717
 Location/Qualifiers

[illegible]

FEATURES									
SOURCE									
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BASE COUNT 199 a 283 c 237 g 148 t 4 others									
ORIGIN									
Query Match	37.8%	Score 513.8	DB 14	Length 871					
Best Local Similarity	80.3%	Pred. Mismatches 155	Indels 8	Gaps 5					
Matches 663	Conservative	0							
6	CCGAGATGAGCGCTTCGGGGCTGCGAGCTTCCCGCTGCTGCCGCTGTGCGCTGC	65							
Db	16	CCCCATGCGCGCTTCGGGGCTGCGAGCTTCCCGCTGCTGCCGCTGTGCGCTGC	75						
QY	66	TAGTCTGACGCTTGGCGCGCGCGCGCGAGCTGTCACATGCAAGACCATGACATGG	125						
Db	76	TAGTCTGACGCGCGCGAGGCGCGCGCGAGCTTCCACATGCAAGACCATGACATGG	135						
QY	126	ACCTGGTGAAGGGGAAGCGCATGAGGCGCATTCGCGCGCGCGAGATTCGTCGAAGCTTC	185						
Db	136	ACCTGGTGAAGGGGAAGCGCATGAGGCGCATTCGCGCGCGCGAGATTCGTCGAAGCTTC	195						
QY	186	TTCGACGCCCCCGAGCCGAGGGGAGCTGCGCGCGCGCGCGCGCGCTGCTGAGGCGAGTCTG	245						
Db	196	TTCGCGAGTCCCCCAGCCGAGGGGAGGAGTACCGCGCGCGCGCGCGCGCGCTGCTGAGGCGAGTCTG	255						
QY	246	CTCTTTACAAAGTACCCGAGCGGGGTAGCGCGGGGAAGTGTGCAACCGGAGCGAGCG	305						
Db	256	CTTTGTACAAAGTACCCGAGCGGGGTAGCGCGGGGAAGTGTGCAACCGGAGCGAGCG	315						
QY	306	CAGAGCGGAGCTACTACGGCCAGAGAGGTACCCCGCTGCTAATGTGGAAGCGGCAC	365						
Db	316	CGAAGCGGAGCTACTATGCTAAAGAGGTACCCCGCTGCTAATGTGGAAGCGGCAC	375						
QY	366	AATCTATGATAATTCAGAGGGGACCCCCACAGCTTATATATGCTGTTCAACACGCGG	425						
Db	376	CAATCTATGATAATTCAGAGGGGACCCCCACAGCTTATATATGCTGTTCAACACGCGG	435						
QY	426	AGCTCCGGGAGGCGGTGCCGGAACCTGTATGTCTCTCGGGCAGAGCTCGCGCTGCTGA	485						
Db	436	ACATTCGGGGAAGAGTGGCCGGAACCCCATGTGCTGCCGTGCAAGAGCTCGCTTGGAGA	495						
QY	486	GGCTCAAGTTAAAGTGTGAGCAGCAGCTGGAGTATACCAAGAAATACGAATGATTCCT	545						
Db	496	GATTTAAATCAAGTGTGAGCAGCAGCTGGAGTATACCAAGAAATACGAATGATTCCT	555						
QY	546	GGCGTACCTCAGCAACCGGCTCTGGCCCCCAGTGACTACCGGAGTGGCTGTCTTTG	605						
Db	556	GGCGTACCTTGGTAAACGGGCTGTGACCCCACTGATAGCCGTAGTGGGTGCTTTTG	615						
QY	606	ATGTCAACCGGAGTTGTGCGGCAGTGCTGACCCGAGAGAGGCTATAGAGGTTTGGCC	665						
Db	616	ACGTCTACTGAGTTGTACGCGAGTGGCTGGAACGAAGAGGAAATACAGGCTTTTCAT	675						
QY	666	TGAGTGGCCACTCTCTCTGTGACGAGCAAGATTAACAC-ACGCCAGTGGAAATTAACGGG	724						

DB	676	TCAGCGCTCACGCTCTCTGTGTGACAGCAACAAAGATATACANAACTCCACCTGGAAATCAACGGN	735
QY	725	TTCAA--TTCTGCGCGCGCGGGGTGACCTGGC-CACCATTTACGGGCATGAA-CCGGCCCT	779
DB	736	GATCAGAGCCCCCAACGTCGGGGGGCGACCTCGGNGACACATTCATGACATGAANACGGCCCT	795
QY	780	TCCTGCTCTCTCATGGC--CAGCCCGCTGGAGAGGGCCCAAGACCTGG	823
DB	796	TCCTGCTCTCTCATGGCAACCCCGCCCTGGAAAGGCCAGACACTGG	841
RESULT 11			
LOCUS	BM469326	1013 bp	mRNA
DEFINITION	AGNCOCURT_6480727 NIH_MGC_85 Homo sapiens	linear	EST 05-FEB-2002
ACCESSION	BM469326		IMAGE:5551510
VERSION	5', mRNA sequence.		
KEYWORDS	BM469326.1	GI:18518368	
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strusberg, Ph.D.		
	Email: c9apbs-remail.nih.gov		
	Tissue Procurement: Lou Staudt		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	plate: LNLMI2265	row: f	column: 23
	High quality sequence stop: 530.		
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	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: lymph; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."		
BASE COUNT	225 a	333 c	291 g
ORIGIN		163 t	1 others
Query Match	37.2%	Score 506.6;	DB 13; Length 1013;
Best Local Similarity	88.9%;	Pred. No. 2.1e-100;	
Matches 559;	Conservative	0; Mismatches 69;	Indels 1; Gaps 1;
QY	6	CCGAGATGCGCCCTTCGGGCGCTCGGCGCTCTTCGCCCTGCTGCCCTGCTGTGGCTGC	65
DB	9	CCCCCATGCGCCCTCGGGCGCTCGGCTGCTCCCTCTGCTACCGCTGCTGGCTAG	68
QY	66	TAGTGTGACGCGCTGGCGCGCGCGCGCGGAGCTGTCCACCTGGAAAGCATGACATGG	125
DB	69	TGGTCTGACGCTTGCGCGCGCGCGCGGAGCTATCCACTGCAAGACTATGACATGG	128
QY	126	AGCTGTGTAAGCGAAGCGCATGAGGCCATTTCGCGGAGATGCTGTCCAAGCTTCGGC	185
DB	129	AGCTGTGTAAGCGAAGCGCATGAGGCCATTCGCGGCGCAATCTGTCCAAGCTTCGGC	188
QY	186	TTGCCAGCCCCCGAAGCCAGGGGAGCTGCGCCCGCGCCCTGCTGCTTAAGCATGACTGG	245
DB	189	TGCGAGAGCCCCCGAAGCGGAGGAGTGTGCGCCCGCGCGCTGCTGCGGAGCGCTGCTG	248

OY	246	CTCTTTAAACAAGTACCGCGCAGCGGGGTAGCGCGGGAAGTGTGGAACCGGACCCGACG	305									
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OY	306	CAGAGCGGAGCTACTACAGCCCAAGGAGGTCCACCCGGTGCTTAATGTTGGAAAGCCGCAAC	365									
DB	309	CTGAGGCCGACTACTACGCCCAAGAGAGTCCACCCGGTGCTTAATGTTGGAAACCCACAGC	368									
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DB	369	AAATCTATGACAAAGTTCAAGCAGAGTACACACAGATATATATGTTCTTCAACATCAG	428									
OY	426	AGCTCCGGGAGAGCGGTGCCGAGACCTGTATTGTCTCTCGGGCAGAGTGGCGCTGCTGA	485									
DB	429	AGCTCCGGGAGAGCGGTACTGTAAACCCGGTGTCTCTCCGGGCGAGAGCTGGCTGTGCGA	488									
OY	486	GGCTCAAGTAAAAATGGAGCAGCAGCTGGAGACTATTACACAAATATACGAAATGTTCT	545									
DB	489	GGCTCAAGTAAAAATGGAGCAGCAGCTGGAGACTATTACACAAATATACGAAATTTCT	548									
OY	546	GGCGCTACCTCAGCAACCGGCTGTGCGCCCAAGTACTACCGAGAGTGGCTGTCTTTG	605									
DB	549	GGCGATACCTCAGCAACCGGCTGTGCGCACCAAGAGACTCGCCAGAGAGTATTCTTTG	608									
OY	606	ATGTACAC-GGAGTGTGTGCGCAGTGGCT	633									
DB	609	ATGTACACCGGAGTGTGCGCAGTGGCT	637									
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DEFINITION	AGNCOCURT.6830409 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936397											
ACCESSION	BO054305											
VERSION	BO054305.1	GI:19813645										
KEYWORDS	EST.											
SOURCE	human.											
ORGANISM	Homo sapiens											
REFERENCE	Munkiyola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;											
AUTHORS	Munkiyola; Eutheria; Primates; Catarrhini; Homiidae; Homo.											
TITLE	NIH-MGC http://mgc.nci.nih.gov/											
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)											
COMMENT	Unpublished (1999)											
	Contact: Robert Strausberg, Ph.D.											
	Email: c9apbs-remail.nih.gov											
	Tissue Procurement: Dr. Daniel MCVicar, DHS/NCI											
	cDNA Library Preparation: Rubin Laboratory											
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)											
	DNA Sequencing by: Agencourt Bioscience Corporation											
	Clone distribution: MGC clone distribution information can be											
	found through the I.M.A.G.E. Consortium/LNL at:											
	http://image.lnl.gov											
	Plate: L1CM2125 row: k column: 22											
	High quality sequence stop: 605.											
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	/tissue_type="natural killer cells, cell line"											
	/lab_host="DH10B (phage-resistant)"											
	/note="Organ: blood; Vector: pOT87; Site:1: XhoI; Site:2:											
	EcoRI; cDNA made by oligo-dT priming, directionally cloned											
	into EcoRI/XhoI sites using the following 5' adaptor:											
	GGCCAGCGAG(G). Library constructed by Ling Hong in the											
	Laboratory of Gerald M. Rubin (University of California,											
	Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and											
	non-superscript II RT (Life Technologies). Note: this is a											
	NIH MGC Library."											
FEATURES												
	source											

BASE COUNT	233 a	347 c	309 g	203 t	1 others
ORIGIN					
Query Match	37.2%; Score 506.6; DB 14; Length 1093;				
Best Local Similarity	82.5%; Pred. No. 2.2e-100;				
Matches 682; Conservative	0; Mismatches 79; Indels 54; Gaps 2;				
OY	535 CATGATTCCTGGCGGCTACACAGACCGGCTCTGGCCCCAGTAGTCACTCCGGAGTG 594				
Db	1 CACACATTCCTGGCGGCTACACAGACCGGCTCTGGCCCCAGTAGTCACTCCGGAGTG 60				
OY	595 GCTGTCCTTTGATGTACACCGGAGTTGTGCGGAGTGTGCTGACCCCGAGAGGCTATAGA 654				
Db	61 GTTATCTTTTGTGATGTACACCGGAGTTGTGCGGAGTGTGAGCCCTGGAGGGGAATTGA 120				
OY	655 GGGTTTCCGCTTACGTAGTCCCACTTCTCTGTGACAGCAAGATAACACTCCACGTGCA 714				
Db	121 GGGCTTTCCGCTTACGTAGTCCCACTTCTCTGTGACAGCAAGATAACACTCCACGTGCA 180				
OY	715 AATTACGGGTTCAATTCTGGCCGCGGGGTGACCTGGCCACCATTCACGGGATGAACG 774				
Db	181 CATCAATGGGTTCAATTCTGGCCGCGGGGTGACCTGGCCACCATTCATGGCATGAACG 240				
OY	775 GCCCTTCCTGCTCCTCATGGCCACCCGCTGAGAGGGCCCAAGACCTGCACAGCTCCG 834				
Db	241 GCGTTTCCTGCTCCTCATGGCCACCCGCTGAGAGGGCCCAAGACCTGCACAGCTCCG 300				
OY	835 GCACCCCGGAGCCCTGGATACCAACAGTACCCATACACGTCGCAAGTACGATCTCT 894				
Db	301 GCACCCCGGAGCCCTGGATACCAACAGTACCCATACACGTCGCAAGTACGATCTCT 310				
OY	895 GGGCCGTGATACCAACTACTGCTTACAGTCCACGGAGAAAGTCTGCTGGCGAGCT 954				
Db	311 -GGCCGTGATACCAACTACTGCTTACAGTCCACGGAGAAAGTCTGCTGGCGAGCT 369				
OY	955 CTACATGTAGCTTCGCGAGAGACCTGGGCTGGAAGTGAATTCATGAACCCCAAGGGCTACA 1014				
Db	370 GTACATGTAGCTTCGCGAGAGACCTGGGCTGGAAGTGAATTCACAGACCCCAAGGGCTACA 429				
OY	1015 TGGCAATTTCTGCTGGGGGCGCTGCTCCCTACATCTGAGAGCCATGACATCAAGCA 1074				
Db	430 TGGCAATTTCTGCTGGGGGCGCTGCTCCCTACATTTTGAAGCCATGACATCAAGCA 489				
OY	1075 GGGCTGAGCTCTGTATACACAGACAAACCCGGGCGCTGGGGGCGCGCTGCTGCC 1134				
Db	490 GGGCTGAGCTCTGTATACACAGACAAACCCGGGCGCGCTGCTGCC 549				
OY	1135 GCAGGGCTGAGGACCACTGCCATCGTGTACTACGTGGGCGCGCAAGCCCAAGGTGAGCA 1194				
Db	550 GCAGGGCTGAGGACCGCTGCCATCGTGTACTACGTGGGCGCGCAAGCCCAAGGTGAGCA 609				
OY	1195 GCGTGTCAACATATATCGTGGTCTGTGCAATGCAAGGAGGCCCCCGCCCGCCACAG 1254				
Db	610 GCGTGTCAACATATATCGTGGTCTGTGCAATGCAAGGAGG---GTCCGCCCCCGCC 666				
OY	1255 CCGGCCACCCGCGAGGCGCGGCCCAACCCCGCGCGCTC 1295				
Db	667 GCCCGCGCGCGAGGCGCGGCCCAACCCCGCGCGGCC 707				

RESULT 13
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 DEFINITION 603070060F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218983 5',
 mRNA sequence.
 ACCESSION B1909079
 VERSION B1909079
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 943)

AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ ;				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: c9aps-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM11550 row: 9 column: 16 High quality sequence stop: 682.				
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	/clone="IMAGE:5218983"				
	/clone_1ib="NIH_MGC_118"				
	/tissue_type="leukocyte"				
	/lab_host="DH10B"				
	/note="Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC library."				
BASE COUNT	170 a	315 c	291 g	166 t	1 others
ORIGIN					
Query Match	37.1%; Score 504.8; DB 13; Length 943;				
Best Local Similarity	80.4%; Pred. No. 5.2e-100;				
Matches 682; Conservative	0; Mismatches 147; Indels 19; Gaps 7;				
OY	6 CCGAGATGGCGCTTCGGGGCTGGGAGCTCTGCGCGCTGCTGCTGCGCTGCGCTGCG 65				
Db	95 CCCCATCCCGCCCTCCGGGCTGGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAC 154				
OY	66 TAGTGTACAGCGCTTGGCGCGCGCGCGCGGACTGTCACTGCAAGACCATGACATGG 125				
Db	155 TGGTGTACAGCGCTTGGCGCGCGCGCGGAGTATCACTGCAAGATATGACATGG 214				
OY	126 AGCTGTACAGCGGAGGCGCATTCGCGGCGGCAAGATTTCTGCCAAGCTTGGCG 185				
Db	215 AGCTGTACAGCGGAGGCGCATTCGCGGCGGCAAGATTTCTGCCAAGCTTGGCG 274				
OY	186 TTGGCAGCCCCCGAGCCAGGGGGAGGTGCGGCGCGCGCGCTGCTGAGGAGTATGG 245				
Db	275 TTGGCAGCCCCCGAGCCAGGGGGAGGTGCGGCGCGCGCGCTGCTGAGGAGTATGG 334				
OY	246 CTCTTTACAGTACCGCGGAGCGGGTACCGGGGAAAGTGTGCAACCGAGCCGAGC 305				
Db	335 CCTGTACAGAGCACCGCGGAGCGGGTGGCGGAGAGTGCAGAAACCGAGGCCGAGC 394				
OY	306 CAGAGCGGAGTACTAGGCA-AGGAGTACACCGCGGTGTATGTGGGAA-CCGCGCA 363				
Db	395 CTGAGCGGAGTACTAGGCAAGGAGTACACCGCGGTGTATGTGGGAAACCGCGCA 454				
OY	364 CCAATCTATGTAATTAATCAAGGACCCCGCACGCTTATATGCTGTTCAACAGCTC 423				
Db	455 CGAATCTATGTAATTAATCAAGGAGTACACGAGTATATATGTTCTTCAACAGCTC 514				
OY	424 GGAGCTCCGGGAGGGGTGCGGAACTTATTTCTCTCGGAGAGAGTGGCGCTGCT 483				
Db	515 AGAGCTCCGAGAGGGGTGCTGAACCGGTGTGCTCTCCCGGAGAGAGTGGCTGCTGCT 574				
OY	484 GAGGCTCAAGTTAAAGTGGAGCAGCTGTGAGTATACAGAAATACAGCAATGATTC 543				
Db	575 GAGGCTCAAGTTAAAGTGGAGCAGCTGTGAGTATACAGAAATACAGCAATGATTC 634				

OY	544	CHGGGGCTACCTCAGCAACCCGGCTGCTGGCCCCAG--TGACTCACGGAGTGGCTGCC	601
Db	635	CTGGGGGAATACCTCAGCAACCCGGCTGCTGGCCCCAGCGAGCATCTCCGCAAGAGTATATCT	694
OY	602	TTTGGATGTCACCGGAGTTGT---GCGGACAGTGGCTGACCCGGACAGAGAGGCTPTAGAGGGT	658
Db	695	TTTGGATGTCACCGGAGTTGTTCGGGCAAGGTGGTGGAGCCGTGGAGGGGACATTGGAGGGC	754
OY	659	TTTGCCCTCAGTGGCCCACTCTTCCG-----CTGACAGCAAGATPACACACTCCACGTG	712
Db	755	TTTCCGCTTAGGGGCCCACTGCTCTTGTCAGCACAGCAGGAGTTAGACACACTCTGCACGTG	814
OY	713	GA--AATTAGAGGGTTCAATTCTGGCCCGCG---CGGTGACTGGCCACCATTTACAGGC	766
Db	815	GACCATTTACAGCGGGTTCACTACCCGGGCGGAGAGGGTGGCCCGCACCATTTCAATGAG	874
OY	767	ATGAACCGGCGCTTCTGCTCTCATATGGCCACCCCGCTGAGAGGGGCCAGCACTCGAC	826
Db	875	CATTGACCGGGGCTTCTGTTCTCAATGGACCCCGCTGGCGCGGCGGCGCTTCTGAC	934
OY	827	AGCTCCCG	834
Db	935	GGCTCCG	942
RESULT	14		
LOCUS	BG748049	821 bp	mrna linear EST 15-MAY-2001
DEFINITION	60270554F01 NIH_MGC_43 Homo sapiens CDNA clone IMAGE:4842275 5',		
ACCESSION	BG748049		
VERSION	BG748049.1	GI:14058702	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 821)		
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapds-remail.nih.gov Tissue Procurement: ARCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LNCMI676 row: g column: 12 High quality sequence stop: 812. Location/Qualifiers 1. 821 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4842275" /clone_lib="NIH_MGC_43" /issue_type="normal pigmented retinal epithelium" /lab_host="DH10B (phage-resistant)" /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA Synthesis Kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NIH_MGC Library. "		
FEATURES	source		
BASE COUNT	152 a	290 c	243 g 136 t
ORIGIN			
Query	Match	36.9%	Score 502: DB 12: Length 821:

[illegible]

